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Application Applic	Applicatio Applicatio
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esquence sequence seq	Sequence
US-08-682- US-08-836- US-08-836- US-08-836- US-08-836- US-08-836- US-08-843- US-08-669- US-08-775- US-08-669-	-80-
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ALIGNMENTS

Sequence 7, Application US/0855424
Sequence 7, Application US/0855424
GENERAL INFORMATION:
APPLICANT: Warmke, Jeffrey W.
APPLICANT: Wan Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCES: 1
ADDRESSEE: Je.O. Box 2000, 126 E. Lincoln Avenue CITY: Rahway
STATE: New Jersey
COMPUTE: New Jersey
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,424
FILING DATE:
CLASSIFICATION: 424 US-08-554-424-7 STANDARD; DNA; UNC; 6513

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                                                                                                             APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
CORRESPONDENCE: 32
CORRESPONDENCE ADDRESS:
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SEQUENCE 6519 BP; 1707 A; 1544 C; 1698 G; 1570 T; 0 OTHER.
                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                      ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
                                                                                                                                                                                                                                                                                                                                                                                                                         19603/1062 (D-1906A)
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Pred. No. 0.00e+00;
                                                         BP
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         Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/034,361
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION UNMBER: US 60/012,649
FILING DATE: 01-MAR-1996
                                             T. 2
US-08-808-793-24 STANDARD; DNA; UNC; 6519
                                                                                                                                                                                                             COUNTRY

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/808,793
                                                                                  Sequence 24, Application US/08808793
Sequence 24, Application US/08808793
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J.
REGISTRATION NUMBER: 34,103
REFRENCE/COCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                TELECHONE: 716-202 TELEBHONE: 716-203 TELEBHONE: 716-263-1600 INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: FNGTH: 6519 base pairs
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al Similarity 97.7%;
6337; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                         CITY: Rochester STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                            USA
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δy	5604	TAAGCTTTTTGATAGTTATTAATATGTACATTGCTGTCATTCTCGAGAACTATAGTCA

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SEQUENCE 5461 BP; 1425 A; 1259 C; 1374 G; 1403 T; 0 OTHER
                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,289
FILING DATE: 30-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                    Company
                                                                                                                                                                              NAME: Harrington, James J.
REGISTRATION NUMBER: P-38,711
REFERENCE/DOCKET NUMBER: 31,732
TELECOMMUNICATION INFORMATION:
TELEFHONE: 201-831-3346
TELEFAX: 201-831-3305
                    Cyanamid
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                             LENGTH: 5461 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     67.28;
96.78;
                   SEE: American C: One Cyanamid Wayne
         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   Query Match 67.2%;
Best Local Similarity 96.7%;
Matches 5445; Conservative
                                                                               COMPUTER READABLE FORM:
                                                 New Jersey
U.S.A.
NUMBER OF SEQUENCES:
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MOLECULE TYPE:
                                                                   ZIP: 07470
                   ADDRESSEE:
STREET: On
                                      CITY: Way
STATE: Ne
COUNTRY:
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 GCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACGACTACGACATGTACTATGAGATC
           5743 ACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAGAGGAGGGGGTGAGATTGGTGAG
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Sequence 7, Application US/07998289
GENERAL INFORMATION:
APPLICANT: Black, Bruce C.
APPLICANT: Taylor, Martin
APPLICANT: Heckel, David G.
TITLE OF INVENTION: Method for Mon
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US-07-998-289-7 STANDARD; DNA; UNC;
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	3TACACGATACGGAA	4 GGTTCACCGTTTAACATACGCAGGGGATCACGTAGTTCTCACA	8 GGACGTGGCCGCTTTGGTATACC	8 CAGGATGCCCAGCAGTTGCCCTATGCCGACGACTCGAATGCCGTCACCGATG		8 GAAGAGAATGGGGGCCATCATAGTGCCCGTGTACTATGGCAATCTAGGCTCCCGACACTC	4 GAAGAGAATGGGGCCATCATAGTGCCCGTGTACTATGGCAATCTAGGCTCCCGACACTCA	8 TCGIATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGGCGGC	4 TCGTATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGGCGG	8 AIGGCCGTCATGGGCGTCAGCACAATGACCAAGGAGAGCAAATTGCGCAACCGCAACACA	4 ATGCCCGTCATGGCCGTCAGCACAATGACCAAGGAGGAGCAAATTGCGCAACGCAACAC	8 CGCAATCAATCAGTGGGCGCCACCAATGGCGGCACCACTGTTTGGACACCAATCACAG	4 CGCAATCAATCAGTGGGCGCCCCACCAATGGCGGCACCACCTGTCTGGACACCCAATCACAA	8 CTCGATCATCGCGACTACGAAATTGGCCTGGAGTGCACGAAGCTGGCAAGATT	4 CTCGATCATCGCGAC	8 CATCATGACAATCCTTTTATGGAGCCCGTCCAGACACAAACGGTGGTTGATATG	4 CATCATGACAATCCTTTTATCGAGCCCGTCCAGACACAAACGGTGGTTGATATGAAAGA	8 GIGATGGTCCTGAATGACATCGAACAGGCCGCTGGTCGGCACACGCGAAGCGAT	4 GIGATGGTCCTGAATGACATCATCGAACAGGCCGCTGGTCGTCGCCACAGCGA	8 CGCGGTGTCTCCGTTTACTATTTCCCAACAGACGACGACGAGGACGAGGATGGCCCGACGTT	4 CGCGGTGTCTCCGTTTACTATTTCCCAACAGACGACGATGACGAGGATGACGCCC	8 AAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGTTTTGTGTGTG	4 AAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGT	8 IGCTGGGTTTGGTTGAAATTTCAGGAGTGGGTATCGCTCATCGTCTTCGATCCCTTCGT	4 IGCIGGETITGETIGAAAITICAGGAGTGGGTATCGCTCATCGTCTTCGATCCCTTC	8 GAGCTCTTCATCACGCTGTGCATTGTGGTCAACACGATGTTCATGGCAATGGATCACCA	4 GAGCICITCATCACGCIGIGIGITI GIGGICAACACGATGTTCATGGCAATGGATCATCA	8 GATATGAACAAGGAGATGGAACGCGTGCTCAAGAGTGGCAACTATTCTTCACCGCCAC	4 GATATGAACAAGGGGAACGCGTGCTCAAGAGTGGCAACTATTTCTTCACCGCCACC	8 TITGCCATCGAGGCCACCATGAAGCTAATGGCCCATGAGCCCCAAGTACTATTTCCAGGA	4 TITGCCATCGAGGCCACCATGAGGTAATGGCCAT	8 GGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT	4 GGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATCGCTATTGGAACTGGGACTCGA	8 GOTGTCCAGGGTCTGTCCGTATTGCGTTCCTTTCGATTGCTGCGTGTATTCAAACTGGCC
1644	99	1704	1678	73	82	1798	1884	1858	194	1918	2004	1978	2064	2038	2124	2098	218	215	224	2218	230	2278	2364	233	242	239(248	245	254	251	260	2578	266	2638
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TGTCCAGGGTCTGTCCGTATTGCGTTCCTTTCGATTGCTGCGGTGTATTCAAACTGGCC STCTTGGCCCACACTTAATTTACTCATTTCGATTATGGGACGCACCATGGGCGCTTTG STCTTGGCCCACACTTAATTTACTCATTTTCGATTATGGGACGCACCATGGGCGCTTTG AATCTGACATTTGTACTTATTACTCATTTATGGGACGCACATGGGAATGCAA AATCTGACATTTGTACTTATCATCTTACATCTTTGCGGTGATTGGAATGCAATGGAATGCAATGACAATGAATG	CIGITCGGAAGAATAICATGATCACAAGGACCGCTTTCCGGATGGCGACCTGCCGGC CTGTTCTCTTCTC	#TCGAGTCCATGTGGGACTGCATGTACGTGGGCGATGTCTCGTGCATTCCCTTCTTC	CCAATTTTGGCTCATCTAGCTTATCAGCGCCGACTGCCGTTACTTTGCTTACCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTGC	GCCGAGGCCTTCAATGGCCGATTTAAAAGTTGGGTTAAGCGTAATGTTGGTGAT [AGGACCAACCAGATCAGTTGGATTTGGAGCGAAGGAACGAAC	GGCCACGACGACATCCTCGCCGACGGCCTCATCAAGAAGGGATCAAGGAGCAGACGCAA 	CTGGAGGTGGCCATCGGGGATGGCATGGAATTCACGATACACGGCGACATGAAGAACAAC	AAGCCGAAGAATCCAAATATCTAAATAACGCAACG	CAAGACAATAGACTGGAACACGAGCTAAACCATAGAGGTTTGTCCTTACAGGACGACGACA	ACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAGGACGAGGCCAC 	AAGGCAGCGCGAGACGATGGAGGGCGAGAGAAGCGCGACGCCAGCAAGGAGGTTTA 	GGTCTCGACGAGGAACTGGACGAGGAGGGGAATGCGAGGAGGGCCCGCTCGACGGTGAT 	ATCATTATTCATGCACACGACGAGGATATACTCGATGAATATCCAGCTGATTGCTGCCCC
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4563 4443 4643 4503 4703 4763 4623 4683 4943 4403 4263 4463 4323 4383 4143 4203 4043 3903 4103 4023 4083 4283 AAGCTCAGCCACGAGATCATACCAAATCGCAATGCCTGCGAGGGGGGGAGAACTACACGTGG CCACTACGTGCCCATGTCCCGTATGCAGGCCATGAGGGTCGTTAATGCGCTGCAACAAA GCCACCTTCAAAGGCTGGATACAAATCATGAACGATGCTATCGATTCACGAGGGGGGAC AAGCAACCAATTCGTGAAACGAACATCTACATGTATTTATATTTCGTATTCTTCATA TTTGGATCATTTTTCACACTCAATCTGTTCATTGGTGTTATCATTGATAATTTTAATGAG TGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAATTCGATATAATCATT CCACAAAGACCCATACTGCAGGATATTTTATACTATATGGACAGAATATTTACGGTTATA GCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTCTAATATTTTGGCTAATTTTTGCC ATAATGGGTGTACAGCTTTTTGCTGGAAAATATTTTAAGTGCGAGGACATGAATGGCACG GCTGTTATCACTATGATTTTAATGAGTAGCTTTAGCTTTGGCATTAGAAGATGTACATCTG TTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTTCGGCTTCAAAGTGTACTTGACCAAC 4524 4644 4704 4564 4764 4624 4824 4684 4884 4504 3864 4044 4224 4284 4144 4344 4204 4404 4264 4464 4324 4384 4584 4444 3924 3784 3984 3844 3904 4104 3964 4164 4024 4084 3664 3724 g qq g g QΫ QQ οy 셤 δ g οy g QΥ g δy ద ò g δ g Q Q Ω g δ Q ద ŏ δý Q 셤 ρý Qγ οy ò

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                                                                                                                                                                                                                                                                                                                                             Indels 177;
                                                                                                                                                                                                                                                                                                                  Length 5461;
                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
SEQUENCE 5461 BP; 1425 A; 1259 C; 1374 G; 1403 T; 0 OTHER.
  PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                Score 4374; DB 11;
Pred. No. 0.00e+00;
0; Mismatches 9;
                                                                   ATTORNEY/AGENT INFORMATION:
NAME: ROLINSON, JOSEPH R
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/0A939
TELEPHONE: 212-527-7700
TELEPHONE: 212-753-6237
                           APPLICATION NUMBER: US/07/998,289B
                                          30-DEC-1992
                                                                                                                                                                 TELEX: 236687
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 5461 base pairs
                CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                               Query Match 67.2%;
Best Local Similarity 96.7%;
Matches 5445; Conservative
                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                          linear
                                          FILING DATE: 3(CLASSIFICATION:
                                                                                                                                                                                                                                                          TOPOLOGY:
  SOFTWARE:
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              4984 TACTICGIGICGCCGACCCIGCICCGAGIGGIGCGIGIGGCGAAAGIGGGCCGIGICCII
                                                                                                                                                                                                                                          CCGGCCCTGTTCAACATCTGCCTGCTGCTGCTCCTGGTCATGTTCATCTTTGCCATTTTC
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                                                       ACGTATAACGCGGTCCTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGTTCCGAA
                                                                                                             GGTGTACTGGACGCCATTATCAATGAGGAAGCATGCGATCCACCCGACAACGACAAAGGC
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APPLICANT: Taylor, Martin
APPLICANT: Taylor, Martin
APPLICANT: Heckel, David G
TITLE OF INVENTION: Method for Monitoring Pesticide
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JT 4
US-07-998-289B-7 STANDARD; DNA; UNC;
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Sequence 7, Application US/07998289B
GENERAL INFORMATION:
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721 ACGITTAGGGIGCIGCGAGCGCITAAAACCGIAGCCAITGIGCCAGGCITGAAGACCAIC 780	901 IGCATCAAGAAGTICCCGCTGGACGGTCCTGGGGCAATCTGACCGAGGAACTGGGAC 960	GGTCCGAATCCGAATTATGGCTACACCAGCTTCGTTCGTT	1224 GCCGGACCATGGCACATGCTGTTATAGTCATCTTCTAGGTTCATCTTTTTTTT	1381 GCGCCAAGCAGCGCCAATGCGCAGCCTAGCGCAGCAGCGGATGCGGCTGCC 1400	ATTCGGAGCGTCGAGGTCGAGTCGGTGAGCGTTATACAAAGACAACCAGCACT 1
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GGCCCACACTTAATTTACTCATTTCGATTATGGGACGCACGATGGGCCTTTG AACATCTTCGACTTCATTATCGTGGCCCTATCGCTATTGGAACTGGGACTCGAG AGGGTCTGTCCGTATTGCGTTCCTTTCGATTGCTGCGTGTATTCAAACTGGCC GAAAGAATTATCATGATCACAAGGACCGCTTTCCGGATGGCGACCTGCCGCGC ATGGGGCCATCATAGTGCCCGTGTACTATGGCAATCTAGGCTCCCGACACTCA :ATCGCGACTACGAAATTGGCCTGGAGTGCACGGACGAAGCTGGCAAGATTAAA BACAATCCTTTTATCGAGCCCGTCCAGACACAAACGGTGGTTGATATGAAAGAT TCATCACGCTGTGCATTGTGGTCAACACGATGTTCATGGCAATGGATCACCAC AATCAGTGGGCGCCACCAATGGCGGCACCACCTGTCTGGACACCAATCACAAG STTTGGTTGAAATTTCAGGAGTGGGTATCGCTCATCGTCTTCGATCCCTTCGTC ACAAGGAGATGGAACGCGTGCTCAAGAGTGGCAACTATTTCTTCACCGCCACC **ITCGAGGCCACCATGAAGCTAATGGCCATGAGCCCCAAGTACTATTTCCAGGAG** TGACATTTGTACTTTGCATTATCATCTTCATCTTTGCGGTGATGGGAATGCAA

	3844 CCA 		4104 TTC	4164 GCG	4024 CTT		4084 CCA 111 4284 CCA			4204 ATA		4264 AAG			4384 GCC	4584 GCC	4444 AAG		4504 TTT 					4684 TGG		4744 ATG			4864 TGT	5064 TGI
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	TGGAACTTCACCGACTTTATGCACAGCTTCATGATCGTGTTCCGGGTGCTCTGCGGAGAA 	TGGATCGAGTCGATGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG	CGTGCATTC	TIGGCCACCGITGICATCGCAATCITGIGGTACTIAAACCITIICITAGCCITITG 	ACGATACGA		GCCGAGGCCTTCAATCGAATTGGCCGATTAAAAGTTGGGTTAAGCGTAATATTGCTGAT	AGCGTAATA	TGTTTCAAGTTAATACGTAACAAATTGACAAATCAAATAAGTGATCAACCATCAG 	-AGCATGGTGACAACGAACTGGAGCTG		GGCCACGACGAGGACCCCGACGGCCTCATCAAGAAGGGGATCAAGGAGCAGACGAA	GGCCACGACGAGCTCGCCGACGGCCTCATCAAGAAGGGGATCAAGGAGCAGACGCAA	CTGGAGGTGGCCATCGGGGATGGCATGGAATTCACGATACACGGCGACATGAAGAACAAC	GCGACATGA	AASCCGAAGAATICCAATTTTTAAATTAACGCAACG	9		ACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAGGACGACCAC	TCAAGGACG	AAGGGCAGCGCCAGACGATGGAGGGCGAGGAGGCGCGACGCCAGCAAGGAGGTTTA	aagggcagcgccgagacgarggaggggagaaaggggggaggaggaggaggaggagarggagartta	GGTCTCGACGAGGAGGACGAGGAGGGGGAATGCGAGGAGGGCCCGCTCGACGGTGAT 	GGICICOCONOGRACIOGRACOROCOCARIOCOCARAGORAGOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOC		GATTCGTACTATAAGAAATTTCCGATCTTAGCCGGTGACGATGACTCGCCGTTCTGGCAA	ACTCGCCGT	GGNIGGGGCAAITIACGACIGAAACIITICGAITAATIGAGGAIAAATAITIGAAACA 	TAGAAGATG	
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	GCTTCATGA	TGTACGTGG	TGTACGTGG	TTGTGGTAC	CAGCGCCGA	CAGCGCCGP	GATTTAAA	GATTTAAA	TGACAAATC		GGAGCGAAG	GCCTCATCA	GCCTCATC	TEGRATICA 	TEGARITO	ATAACGCAA ATAACGCAA		TAAACCAT	GCCATAAGA	AGCCATAAGA	SGCGAGGAGA	GCGAGGAG	SAGGGCGAAT	SATATACTCC	SATATACTCC	ATCTTAGCCC	ATCTTAGCCC	ACTITICGAD	AGTAGCTTAC	
	TTATGCACA	GGGACTGCA	GGGACTGCA	TCGGCAATC	CTAGCTTAT	CTAGCTTAT	GAATTGGCC	GAATTGGCC	GTAACAAAT		GTTGGATTT	TCGCCGACG	TCGCCGACG	GGGATGGCA	ASST PASSOS	AAGCCGAAGAATCCAAATATCTAAATAACGCAACG AAGCCGAAGAATCCAAATATCTAAATAACGCAACGAT		SACACGAGO	CATATGGTA	CATATGGTA	CGATGGAGG	CGATGGAGG	TGGACGAGG	ACGACGAGG	ACGACGAGG	AAATTTCCG?	AAATTTCCG	GACTGAAAA 	ATTTTAATG	
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151 ATACGATATGATGACGAGGACGAAGATCAAGGTCCACAGCCGGATCCCACACTTGAACAG 210
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                                                                                                                                                                                                                                                    Indels 84;
                                                                                                                                                                                                                           Length 6318;
                                                                                                                                                                                  MOLECULE TYPE: cDNA
SEQUENCE 6318 BP; 1713 A; 1341 C; 1597 G; 1667 T; 0 OTHER.
                     NAME: Braman, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEPHONE: 716-263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6318 base pairs
                                                                                                                                                                                                                       Query Match 56.4%; Score 3676; DB 21;
Best Local Similarity 84.9%; Pred. No. 0.00e+00;
Matches 4986; Conservative 0; Mismatches 806;
            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                           single
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CLASSIFICATION:
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Sequence 1, Application US/08808793
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Soderlund, David M.
APPLICANT: Soderlund, David M.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: ADD USE THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon, Hargrave, Devans & Doyle LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5404 ATAAGCTTTTTGATAGTTATTAATATGTACATTGCTGTCATTCTCGAGAAC 5454
                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,361
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 60/012,649
FILING DATE: 01-MAR-1996
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US-08-808-793-1 STANDARD; DNA; UNC; 6318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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8 8	1291 G 1347 G	AAAGGCTICCCGAGGAGGAGGCGTTACGAGAAGCTGAAGAACGGGCAGCAGCCAAGGC 	350 406
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8 8	707 T	CACCGTTTAACTACGCGGGGGGTAACGTTCACACAGGGTACACATTGACATTGACATTGGGGGGGG	766
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2403 2283 2343 2471 2463 2531 2523 2583 2703 2763 2883 2943 3011 3003 3123 2114 2127 2187 2247 2291 2411 2651 TACTICCAGGAAGGCIGGAACAITITCGAITICATIAITGIGGCCITGICICICGCIGGAA 2643 ATGGGTGCATTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCATCTTTGCGTG 2823 2591 CTGGGACTCGAGGGTGTCCAGGGTCTGTCGTATTGCGTTCCTTTCGATTGCTGCGTGT 2771 GATGCCAATCACAAGGAAAAGGGATTATGAAATGGGTCAGGATTATACAGACGAGGT GGCAAAATAAAACACCACGACAATCCTTTTATCGAGCCCGTCCAAACTCAAACAGTGGTA -----AGGACGATGACGAAGAT GTAIGGGACTGTTGGTGTGTGTTTAAAATTTCAGGAATGGGTGTCCTTTATTGTGTTTC GATCCATTCGTGGAGCTCTTCATTACCCTGTGTATTGTGGTCAATACGATGTTTATGGCC ATGGATCATCACGACATGAATCCGGAATTAGAGAAGGTGCTGAAAAGTGGTAATTTC TTCACGGCCACTTTTGCAATTGAAGCCAGCATGAAACTGATGGCCATGAGCCCGAAGTAC TTGGGCCTGGAGGGTGTCCAGGGCCTGTCGGTGTTGAGAAGTTTTCGTTTGCTTCGTGTA ATGGGAATGCAACTTTTCGGAAAGAACTATATTGACCACAAGGATCGCTTCAAGGACCAT GAATTACCGCGCTGGAACTTCACCGACTTCATGCACAGCTTCATGATTGTGTTCCGAGTG GCTTTGCTTTTGTCCAACTTCGGTTCATCTAGTTATCAGCCCCGACTGCCGACAATGAT GACATGAAAGATGTTATGGTCTTAAATGATATCATTGAACAAGCCGCTGGTCGGCATAGT GGTCCCACATTCAAGGACATCGCCCTCGAATACATCCTAAAAGGCATCGAAATCTTTTGT CGTGCTAGTGAACGAGGTG-2115 2232 2248 2292 2284 2352 2344 2412 2404 2472 2464 2532 2524 2592 2584 2652 2644 2712 2772 2832 2824 2892 2884 2952 2944 3012 3004 3072 3064 2067 2068 2128 2172 2188 2704 2764 g g 셤 g g g g g g рp g g g g g g δ ò Q à ŏ ò ò ద δ 셤 δ ò οy ò Ω δ ç δ ò ò

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9 Y	3244	CCATCAG3-A-A-CATGGCGAT-AATG 3265 	
g	3266	-AACTGGAGTTGGGTCATGACGAAATCATGGGCGATGGCTTGATCAAAAAGGGTATGAAG 3324 	
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ολ	3432	GAGCAGACGCAACTGGAGGTGGCCATCGGGATCGGATTGGAATTCACGATACACGGCGAC 3491	
dy Qy	3385	ATGAAAACCAACCAAGCCGAAGAATCAAAATTCATGAACAACAACGATGATTGGAAAC 3444 	
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3 6	06	USCUCETTITESCAMEGGATGGGGCAATTTACGALTGAAAAACTITICAATTAATTGAAAAATTACGCGTTCTGGCAAGGATGGGGCAATTTACGACTGAAAACTTTTCAATTTGAAAAT 396	
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5108 5168 5288 4808 4868 4928 4988 5048 5064 5124 5184 4884 4944 5004 4404 4464 4568 4524 4584 4688 4704 4764 4824 ATTCCAAGACCGAGGTGGCGACCACAAGCAATAGTATTCGAAATAGTTACAGATAAAAAA TACGACGCCTCCGAGGCGTACAACAATGTCCTCGACAAACTCAATGGGATATTCGTAGTT ATTTTCAGTGGCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTATTTCAAAGAG CCATGGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTCAGC GACATCATTGAGAAGTATTTCGTATCGCCGACACTGCTCCGTGTGGTGAGAGTGGCCAAA GTGGGTCGTGTCCTGCGTTTAGTCAAGGGTGCCAAGGGTATCCGGACGTTGCTGTTCGCG CTGCGCGCCCTAAGGCCATTGCGTGCTGTCTCTAGATGGGAGGGTATGAAAGTTGTCGTG TGGCTTATTTTTGCCATTATGGGAGTACAGCTTTTTTGCTGGAAAATATTTTAAGTGTAAA TGTCTATTTCAAGTGGCCACCTTTAAGGGCTGGATCCAGATTATGAACGATGGCCATTGAT TCACGAGAGGTGGACAAGCAGCCGATCCGAGAACCAATATCTACATGTATTTATATTTC GATAATTTTAATGAACAAAAGAAGCTGGTGGATCATTAGAAATGTTCATGACAGAA TICGATATAATCATTATGITGITCATIGGCTTAAACAIGITTACCAIGACCCTCGATCGG GATGGTAATGACACTGTGCTGAGCCATGAAATCATACCGAATCGTAATGCCTGCAAAAGT GAAAACTACACCTGGGAAAATTCGGCAATGAACTTCGATCATGTAGGTAATGCGTATCTC GATCAGAAAAAGTACTATAATGCTATGAAAAAATGGGCTCTAAAAAAACCATTAAAAGCC 4929 5049 5289 4749 4869 4989 4945 5109 5065 5169 5125 5229 5185 4765 4825 4885 5005 4269 4225 4329 4285 4389 4345 4449 4405 4509 4465 4569 4525 4629 4585 4689 4645 4705 4809 4165 g Q g δý Dp δλ g οy g ă g δy g ΟŸ g δy g δŽ g ŏ g δ g δ qq οy g ò à g δ δ a Qγ g QY

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                                                                                                                                                                                                                                                                                                                                                           Length 6318;
                                                                                                                                                                                                                                                                                                                                 T; 0 OTHER
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                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,618
FILING DATE: 01-WAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Branan, Susan J.
NAME: REPRATION NUMBER: 14,103
REFERENCE/DOCKET NUMBER: 19603/601(CRFD-1657)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1600
INFORMATION FOR SEQ ID NO: 1:
                #1.30
                                                                                                                                                                                                                                                                                                                                                        Score 3676; DB 20;
Pred. No. 0.00e+00;
0; Mismatches 806;
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
SEQUENCE 6318 BP; 1713 A; 1341 C; 1597 G; 1667
                Release #1.0, Version
                                            APPLICATION NUMBER: US/08/772,512A
                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 6318 base pairs
                              DATA:
                                                                                                                                                                                                                                                                                                                                                          Query Match 56.4%;
Best Local Similarity 84.9%;
Matches 4986; Conservative
                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
              SOFTWARE: Patentin
  OPERATING SYSTEM:
SOFTWARE: Patent
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                                                        FILING DATE
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APPLICANT: Knipple, Douglas C.
APPLICANT: Ingles, Davidas C.
TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LIP
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                                                                     5409 GACGICIACAACIITCAAGACCIITIGGCCAGAGCAIGAICCIGCICIITICAGAIGICGGACG
                                                                                                                                                                                     CAGCTGTCCGAGTTTCTGGACGTGCTGGAGCCGCCGCTGCAGATCCACAAGAGCGAACAAG
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                                                                                                                             5485 CTTTCATATCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTGTCATTCTC
                                                      5305 GCTGTGTATATTTTAAGACATTTGGCCAAAGTATGATATTGCTGTTTCAGATGTCTACC
                                                                                                              5365 TCAGCCGGTTGGGATGGTGTGTTAGATGCCATTATCAATGAGGAAGATTGCGATCCACCC
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STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-772-512A-1 STANDARD; DNA; UNC; 6318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08772512A Sequence 1, Application US/08772512A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CTGTCGGTGTTCGCGCTGATGGGCCTACAAATCTAT 	ATTAAACGATTCCCCTGGACGGCAGTTGGGGCAATC	CACAATAGCAACAGTTCCAATTGGTTTACGGAGAACA 	GGGAATGTATCCGGTGCGGGACAATGCGGCGAGGATTACGTCTGCCTGC	CAATCC 	TCGTCTCATGACCCAAGATTTCTGGGAGGATC1 	GGACCCTGGCACGTGTTCTTTATAGTCATCATCTTCCTAGG	TTGATTTTGG TTGATTTTGG	SAGGCTGCCGAGGAGGCGATACGAGAAGC 	GCCAAACTGGAGGAGGGCCAATGTAGCAGCTCAAGGGG 	GCTGCGCAGCTCTGCATCCCGAGATGGCAAAGAGT 	GAACTGTTTGTTGGCGGCGAGAAGG 	CGCAGCGTCGAAGTGGAATCGGAGTCGGTGAG 	ACAGCAC-CCGCTACTAAAGTCCGTAAAGTTAG 	TCACCATTTAACCTACGCCGGGGATCACGTAGT 	CGTGGACGTTTTGGTATACCAGGTAGCGATCGCAAGC	GATGCCCAGCAGCATTTGCCCTATGCCGATGACTC	GAGAATGGTGCCATTATAGTACCAGCCTACTATTG	TATACCTCGCATCAATCAAGAAT
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2403 2523 2583 2643 2711 2703 2771 2763 2823 3011 2471 2463 2283 2343 2411 2531 2591 2651 2006 2067 2171 2187 2247 2007 2114 2127 2231 2291 TIGGGCCTGGAGGGTGTCCAGGGCCTGTCGGTGTTGAGAAGTTTTCGTTTGCTTCGTGTA TICAAATIGGCAAAATCAIGGCCCACACICAATITACICATITCGAITAIGGGCCGGACA ATGGGTGCATTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCATCTTTGCCGTG ATGGGAATGCAACTTTTCGGAAAGAACTATATTGACCACAAGGATCGCTTCAAGGACCAT GAATTACCGCGCGTGGAACTTCACCGACTTCATGCACAGCTTCATGATTGTGTTCCGAGTG TACTTCCAGGAAGGCTGGAACATTTTCGATTTCATTATTGTGGCCTTGTCTGTGGGAA GGCAAAATAAAACACCACGACAAATCCTTTTATCGAGCCCGTCCAAACTCAAACAGTGGTA -----AGGACGATGACGAAGAT GGTCCCACATICAAGGACATCGCCCTCGAATACATCCTAAAAGGCATCGAAATCTTTTGT GTATGGGACTGTTGTTGGGTGTGAAATTTCAGGAATGGGTGTCCTTTATTGTGTTC GATCCATTCGTGGAGCTCTTCATTACCCTGTGTATTGTGGTCAATACGATGTTTATGGCC ATGGATCATCACGACATGAATCCGGAATTAGAGAAGGTGCTGAAAAGTGGTAATTTC TTCACGGCCACTTTTGCAATTGAAGCCAGCATGAAACTGATGGCCCATGAGCCCGAAGTAC AATCAATCAATCGGTGCTGCAACCAATGGTGGCAGTAGTACGGCTGGTGGTGGCTATCCC GATGCCAATCACAAGGAACAAAGGGATTATGAAATGGGTCAGGATTATACAGACGAAGCT CGTGCTAGTGAACGAGGTG-----2172 2232 2248 2352 2412 2404 2472 2464 2592 2652 2644 2712 2704 2772 2764 2832 2824 2892 2884 2952 2944 2344 2532 2524 2584 2068 2128 2188 2284 1948 2007 2008 2067 1947 g Q ò g 셤 δ g ŏ g g g g ò ŏ Ω 8 δ ò δ g δ g ΩŸ g δ 엄 δ 쉽 à g ò 셤 δy 8 ò 5

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) CTCTGCGGAGAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGGGATGTCTCGTGC	ATACCCTTCTTGGCCAGGTCGTGATAGGCAATCTTGTGGGTTCTTAATCTTTTCTTA	GCTTTGCTTTTGTCCAACTTCGGTTCATCTAGTTTATCAGCCCCGACTGCCGACAATGAT	ACCAATAAAATAGCAGAGGCCTTCAATCGTATTGCTCGTTTTAAGAACTGGTGAAACGT	AATATTGCCGATTGTTTAAGTTAATTCGAAATAAATTGACAAACAA			AACTGGAGTTGGGTCATGACGAAATCATGGGCGATGGCTTGATCAAAAAGGGTATGAAG 	5 GGCGAGACCCAGCTGGAGGTGGCCATTGGCGATGGCATGGAGTTCACGATACATGGCGAT	ATGADAAACAACCAGCGGAAGAAATTAAAATTCATGAACAACAACGATGATGGAAAC	2 ATGAAGAACAACAAGCCGAAGAAATCCAAATATCTAAATAACGCAACGATGATTGGCAAC	5 TCAATAAACCACCAAGACAATAGACTGGAACATGACCTAAACCATAGAGGTTTGTCCATA	5 CAGGACGATGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG 		2 GACGAGAGCCACAAGGCCAGAGACGCCGAGACGATGGAGGCGGAGGAGGAGGAGGAGGAGGAGGGCGAGGCCAGG	5 AAAGAGGACCTCGGCCTCGACGAACTGGACGAGGGGGGGG	CTGGATGGTGACATTATCATTCATGGCGAAAACGACGACGAGATAATCGACGACTATCCG	GCCGACIGITICCCCGACICGIACIACAAGAAGITICCGAICTIGGCCGGCGACGAGGAC	9 GCTGATIGCTGCCCCGATICGTACTATAAGAAATTTCCGATCTTAGCCGGTGACGAIGAC	5 TCGCCGTTCTGCCAAGGATGGGCCAATTTACGACTGAAAACTTTTCAATTGAAAAT	5 AAAIATTITGAAACCGCAGTIAICACTAIGATTITAAIGAGTAGCITAGCTTIGGCCTIA		5 GAAGAIGITCATTIACCCGAICGACCIGICAIGCAGGAIAIACIGIACIACIACAIGGACAGG	S ATATTTACGGTGATATTCTTTTGGAGATGTTGATCAAATGGTTGGCCCTGGGCTTTAAG	9 AIATITACGGITATATICTICTIGGAAATGTTAATCAAGTGGTTGGCGCTCGGCTTCAAA
3012	3004	3064	3124	3184	2 4	31	3266	3325	3385	3492	3445	3505	56	29	3625	3685	3745	3849	3805	3865	96	392	3985	4089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6318;
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
SEQUENCE 6318 BP; 1713 A; 1341 C; 1597 G; 1667 T; 0 OTHER.
                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US47 ...

FILING DATE:

CLACCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 3676; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/602
TELECOMMUNICATION INFORMATION:
TELEPENONE: 716-263-1304
TELEFAX: 716-263-1600
FORMATION FOR PARTICULAR PORMATION PROPERTY.
                         ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 24-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               LENGIH: 6318 base pairs
                                                                                                                                                                                                                                NAME: Goldman, Michael
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.4%;
Best Local Similarity 84.9%;
Matches 4986; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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New York
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                COUNTRY:
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Sequence 1, Application PC/TUS9724256
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
TITLE OF INVENTION: FLIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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                                                                        ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCGCAAGGGTAATCCGATCGAGGGAGACG
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STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
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AC XXXXXX
DT
C Sequence 1, Application PC/TUS9724256
CC Sequence 1, Application PC/TUS9724256
CC GENERAL INFORMATION:
CC TITLE OF INVENTION: INSECT SODIUM CHANNEL
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC STREET: Clinton Square, P.O. BOX 1051
CC CITY: Rochester
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CTTCATGATTGTGTTCCGAGTG 2943	GCCCGACTGCCGACAATGAT 3123 	AAATTGACAAATCAAATAAGTGACCAA 3243	GAGTTCACGATACATGGCGAT 3384	CATAAGAATCGACCATTCAAG 3564 [CTACAAGAAGTTTCCGATCTTGGCCGCGAGGAC 3804 [
GAATTACCGCGCTGGAACTTCACCGACTTCATGCACACATTGTGTGTG	GCTTTGCTTTTGTCCAACTTCGGTTCATCTAGTTTATCAGCCCCGACTGCCCGACTGCCCGACTGCCTGTGTTGTTTTGTCCAACTTGCCTCATCTAGCTTATCAGCGCCGACTGCCCGACTGCTAGCTTATCAGCGCCGACTGCCCACTAGCTTATCAGCGCCGACTGCCTAGTTGCCTCGTTTTAAAAATAGAACTGGCTCAATCGTATTGCTCGTTTTAAAAACTGGCTTCAATCGTATTGCCGGTTTTAAAAATAGAACTGGCAAGTTGGCCGAATTAAAAATAGCCGAAGCCTTCAATCGAATTGGCCGGATTTAAAAAGTTGGC	AATATTGCCGATTGTTTAAGTTAATTCGAATAAATTGACAAATCAAATAA [CGAT 	CAGGACGATGACACTGCCAGCATTAACTCCATATGGTAGCCATAAGAATCGACCATTCAAG [GCGACTGTTTCCCGGACTCGTACTACAAGAAGTTTCCGATCTTGGCCGGCGACGAGGAC
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5048 4044 4104 4208 4164 4268 4224 4328 4284 4388 4344 4448 4404 4508 4464 4568 4524 4628 4584 4688 4644 4748 4704 4808 4764 4868 4824 4928 4884 4944 5004 5108 5064 GTTTACTICACCAATGCCTGGTGTTGGCTGGATTTCGTGATTGTCATGCTATCGCTTATA 4285 IGGCTTATTTTGCCATTATGGGAGTACAGCTTTTTGCTGGAAAATATTTAAGTGTAAA 4389 TGGCTAATTTTTGCCATAATGGGTGTACAGCTTTTTGCTGGAAAATATTTTAAGTGCGAG 4809 GATCAGAAAAAGTACTATAAATGCTATGAAAAAGATGGGCTCTAAAAAAACCATTAAAAAGCC CCATGGAATTTATTTGATGTAGTAGTTGTCATTTATCCATCTTAGGTCTTGTACTCAGC ATAITIACGGTGATAITCTITITGGAGAIGTTGATCAAAIGGTIGGCCCTGGGCTTIAAG AATTTGGTTGCCGTTTGGTCGGGCTTAAATGATATAGCCGTGTTTAGATCAATGCGCACA TCACGAGAGGTGGACAAGCAGCCGATCCGAGAAACCAATATCTACATGTATTTATATTTC GATAATTTTAATGAACAAAAGAAGAAGCTGGTGGATCATTAGAAATGTTCATGACAGAA ATTTTCAGTGGCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTATTTCAAAGAG CTGCGCGCCCTAAGGCCATTGCGTGCTGTCTCTAGATGGGAGGGTATGAAAGTTGTCGTG 4269 TTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCAGGGCATGAGGGTCGTCTT GATGGTAATGACACTGTGCTGAGCCATGAAATCATACCGAATCGTAATGCCTGCAAAAGT GAAAACTACACCTGGGAAAATTCGGCAATGAACTTCGATCATGTAGGTAATGCGTATCTC TGTCTATTTCAAGTGGCCACCTTTAAGGGCTGGATCCAGATTATGAACGATGCCATTGAT GATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCCATTAAAAGCC ATTCCAAGACCGAGGTGGCGACCACAAGCAATAGTATTCGAAATAGTTACAGATAAAAA TTCGATATAATCATTATGTTGTTCATTGGCTTAAACATGTTTACCATGACCCTCGATCGG 4885 TACGACGCCTCCGAGGCGTACAACAATGTCCTCGACAAACTCAATGGGATATTCGTAGTT 4029 4345 4509 4465 4525 4629 4705 4765 4869 4929 4945 3982 4089 4045 4149 4105 4209 4165 4405 4645 4825 5049 5005 ద ρý a οy g δ g QΥ g òγ QQ οy g δy 8 8 8 8 Oy Dp OY Db QΥ Oy Oy g Q g ÓΫ 요 δ g Qγ g ò ò

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Pred. No. 0.00e+00;
0; Mismatches 812; Indels 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
SEQUENCE 6315 BP; 1711 A; 1344 C; 1595 G; 1665 T; 0 OTHER.
                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                           DOYLE
TITLE OF INVENTION: FLIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DO:
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US97/24256
                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/772,512
FILING DATE: 24-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEFAN: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6315 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                          NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 196
                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 56.3%;
Best Local Similarity 84.8%;
Matches 4980; Conservative
                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                              FILING DATE:
                                                                                                        14603
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Sequence 2, Application PC/TUS9724256
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
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APPLICANT: Soderlund, David M.
APPLICANT: Soderlund, David M.
APPLICANT: Knipple, Douglas C.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
TITLE OF INVENTION: FLIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: P.O. BOX 1051, Clinton Square
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Pred. No. 0.00e+00;
0; Mismatches 812; Indels 84;
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SEQUENCE 6315 BP; 1711 A; 1344 C; 1595 G; 1665 T; 0 OTHER
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,512A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19603/601(CRFD-1657)
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 6315 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Braman, Susan J.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                         Floppy disk
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Best Local Similarity 84.8%;
Matches 4980; Conservative
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CITY: Rochester
STATE: New York
Sequence 2, Applicatic
Sequence 2, Applicatic
GENERAL INFORMATION:
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4808 4868 4268 4524 4584 4688 4644 4704 4764 4824 4284 4404 4464 GTCTACTTCACCAATGCCTGGTGTTGGCTGGATTTCGTGATTGTCATGCTATCGCTTATA 4104 TGGCTTATTTTGCCATTATGGGAGTACAGCTTTTTGCTGGAAAATATTTTAAGTGTAAA GAAAACTACACCTGGGAAAATTCGGCAATGAACTTCGATCATGTAGGTAATGCGTATCTC TGTCTATTTCAAGTGGCCACCTTTAAGGGCTGGATCCAGATTATGAACGATGCCATTGAT GATAATTTTAATGAACAAAAGAAGAAGCAGGTGGATCATTAGAAATGTTCATGACAGAA GATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAAACCATTAAAAAGCC AATTTGGTTGCCGTTTGGTCGGGCTTAAATGATATAGCCGTGTTTAGATCAATGCGCACA CTGCGCGCCCTAAGGCCATTGCGTGCTGTCTTAGATGGGAGGGTATGAAAGTTGTCGTG GATGGTAATGACACTGTGCTGAGCCATGAAATCATACCGAATCGTAATGCCTGCAAAAGT GTATICITCATATATATIGGAICATITITCACACTCAATCTGTICATIGGTGTTATCATI GAAGATGTTCATTTACCCGATCGACCTGTCATGCAGGATATACTGTACTACATGGACAGG 4749 4269 4329 4389 4465 4569 4525 4629 4585 4689 4645 4705 4089 4149 4105 4209 4165 4225 4285 4345 4449 4405 4509 4029 4045 3745 3849 3805 3909 3865 3969 3925 3985 g 8 유 g g g 9 g & 9 5 7 ά Š δý ò Š Д \succ ð ð ₹ ð ž q ₹ ð ⋩ ð **≵** 8 ⋩ 9 ζ ζ

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AAGGATATITITCGTTTTTCTGCCTCAAAAGCAATGTGGCTGCTCGATCCATTCAATCCG 390
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                                                                                    Sequence 2, Application US/08808793
Sequence 2, Application US/08808793
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCTUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SOURCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 3664; DB 21; Length 6315;
Pred. No. 0.00e+00;
0; Mismatches 812; Indels 84;
  MOLECULE TYPE: CDNA
SEQUENCE 6315 BP; 1711 A; 1344 C; 1595 G; 1665 T; 0 OTHER.
                                                                                                                                                                                                                                                                   COMPUTER: LAWPY DISK
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
RPLING DATE: US/08/808,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19603/1062 (D-1906A)
                                                                                                                                                                                          Doyle
                                                                                                                                                                                     ADDRESSEE: Nixon, Hargrave, Devans & STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                              US 60/012,649
                                                       DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE, DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6(
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 6315 base pairs
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Best Local Similarity 84.8%;
Matches 4980; Conservative
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MEDIUM TYPE: Floppy
                                                       STANDARD;
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US-08-808-793-2
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                                                      ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCGCAAGGGTAATCCGATCGAGGAGACG
                                                                                                                                           GACATCATTGAGAAGTATTTCGTATCGCCGACACTGCTCCGTGTGGGGGAGTGGCCAAA
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                                                                                    ATTITCAGIGGCGAATGICTATIAAAAATATICGCTITACGATATCACTATITCAAAGAG
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                                          TACGACGCCTCCGAGGCGTACAACAATGTCCTCGACAAACTCAATGGGATATTCGTAGTT
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OY 1467 GAAGAGGCTGCACTGCATCCGGAA Db 1471 GAACTGTTTGTTGGCGGCGAGAA 1527 GAGCTATTGTTGCGGGCGAGAA Db 1531 CGCACGTCGAAGTGGAATCGGAG Db 1531 CGCACGTCGAGTGGAATCGGAC Db 1591 ACAGCAC-CCGCTACTAAAGTC Db 1591 ACAGCAC-CCGCTACTAAAGTC OY 1647 ACAGCACCCCAAGCTAAAAGTC	Db 1648 TCACCATTAACCTACGCCGGGGG	1887 1888 1947 2007 2008 2008	DD 2008 GATGCCAATCAAAGGAAAAAG (y 2115 AATCACAAGCTCGATCATCGC (b) 2128 GGCAAAATAAACACCAGGAAA (y 2172 GGCAAAATAAACACCAGGAAA (p) 2172 GGCAAGATTAAACATCATGACAA (p) 2188 GACATGAAAGATGTTATGGCAAA (p) 2132 GATATGAAAGATGTATGGTCTT7 (q) 2232 GATATGAAAGATGTGTGTCCTCT7	Db 2248 CGTGCTAGTGAACGAGGTG Qy 2292 CGGGCAACGATCGCGGTGTCTCC Db 2284 GGTCCCACATTCAAGGACATCGCC Db 2352 GGCCGACGTTGAAAGGCAAGGC Db 2344 GTATGGGACTTGTTGGTGGTGC Db 2412 GTGTGGACTTTGTTGGTTGGTTG Db 2404 GATCCATTGTGGTGCTTTGT Db 2404 GATCCATTGTGGAGCTCTTCATG Db 2404 GATCCATTGTGGAGCTCTTCATG Db 2464 ATGGATCATCGTGGAGCTCTTCATG Oy 2472 GATCCATTGTGGAGCTCTTCATG Oy 2472 GATCCATTGTGGAGCTCTTCATG Oy 2472 GATCCATTGTGGAGCTCTTCATG Oy 2472 GATCCATTGTGGAGCTCTTCATG Oy 2472 GATCCATTGTGAGAGCTCTTCATG OY 2472 GATCCATCGTCGAGCTCTTCATG OY 2472 GATCCATCGTCGAGCATTGTTGT OY 2472 GATCCATCGTCGAGCATATGAACAA
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AAATGGCCAAGAGTCCGACGTATTCTTGCATCAGCTAT 1526 CAGCCTACTATTGTAATTTAGGTTCTAGACATTCTTCA 1887 TGACCAAAGAGCAAATTGGGCAGTCGCAACACGC SATCACGTAGTTCACACAAGTACACAATACGAAATGGG STAGCGATCGCAAGCCATTGGTACTGCAAACATATCAG **ATGCCGATGACTCGAATGCCGTAACACCAATGTCCGAA ATCCTTTTATCGAGCCCGTCCAAACTCAAACAGTGGTA** CCAATGGTGGCAGTAGGACGGCCGGTGGTGGCTATCCC SGGATTATGAAATGGGTCAGGATTATACAGACGAAGCT TAAATGATATCATTGAACAAGCCGCTGGTCGGCATAGT ------AGGACGATGACGAAGAT TTACCCTGTGTATTGTGGTCAATACAATGTTCATGGCC CGGAATTGGAGAGGTGCTGAAAAGTGGTAACTATTTC PCCGTAAAGTTAGCACGACTTCCTTATCCTTACCTGGT

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APPLICANT: Soderlund, David M.
APPLICANT: Ripple, Douglas C.
APPLICANT: Ripple, Douglas C.
AITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT
TITLE OF INVENTION: HOUSE FLIES
TITLE OF INVENTION: HOUSE FLIES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
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                                                       5889 ATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGGTAGAGGAGGCG
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5829 TACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACTGCGTCGAC
                                     5785 ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCGCAAGGGTAATCCGATCGAGGAGAGG
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PatentIn Release #1.0, Version #1.30
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Pred. No. 0.00e+00;
0; Mismatches 813;
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US-08-608-618-1 STANDARD; DNA; UNC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGIESTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
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larity 84.7%;
Conservative
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CLASSIFICATION: 530
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CITY: RO
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GAATTG(GACCTG(GAATTGCCGCGCTGGAATTTCACCGACTTCATGCACAGCTTCATGATTGTGTTCCGAGTG 2943
CTGTGC 	CIGIGCGGAGAGIGGAIGGAIGCAIGIGGGACIGCAIGIAIGI
ATACCC ATTCCC	ATACCCTTCTTCTGGCCACGGTCGTGATCGGCAATCTTGTGGTTCTTAATCTTTTCTTA 3063
GCTTTGC GCCTTGC	GCTITGCITITGICCAACTICGGITCAICTAGITIAICAGCCCCGACTGCCGACAATGAI 3123
ACCAATA ACGAATA	ACCAATAAAATAGCAGAGGCCTTCAATGGTATTGCTCGTTTTAAGAACTGGGTGAAACGT 3183
AATATT(AATATT(AATATTGCCGATTGTTTAAGTTAATTGGAAATAAATTGACAAATCAAATAAGTGACCAA 3243
CCATCAC	CCATCAG3265
-AACTG 	-AACTGGAGTTGGGTCATGACGAAATCATGGGCGATGGCTTGATCAAAAGGGTATGAAG 3324
GGCGAG	GGCGAGACCCAGCTGGAGGTGGCCATTGGCGATGGAGTTCACGATACATGGCGAT 3384
ATGAAA ATGAAG	ATGAAAACAACAGCCCAAGAAATCAAAATTCATAAACAACGATGATGGTTGGAAAC 3444
TCAATAA TCAATTA	CAATAAACCACCAAGACAATAGACTIGGAACATGAGCTAAACCATAGAGGTTTGTCCATA 3504

CAGGACGATGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG 3612 CAGGACGACGACGCACGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG CTGGATGGTGACATCATCATTCATGCCCCAAAACGACGACGAGATAATCGACGACTATCCG AAAGAGGACCTCGGCCTCGACGAGGAACTGGACGAGGAGGCCGAGGGCGATGAGGGCCAG TGGCTTATTTTTGCCATTATGGGAGTACAGCTTTTTGCTGGAAAATATTTTAAGTGTAAA TGTCTATTTCAAGTGGCCACCTTTAAGGGCTGGATCCAGATTATGAACGATGCCATTGAT GACGAGAGCCACAAGGGCAGCGCCGAGACCATCGAGGGCGAGGAGAAACGCGACGTCAGC AAATATTTTGAAACCGCAGTTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCCTTA GAAGATGTTCATTTACCCGATCGACCTGTCATGCAGGATATATTGTACTACATGGACAGG AATTTGGTTGCCGTTTGGTCGGGCTTAAATGATATAGCCGTGTTTAGATCAATGCGCACA CIGCGCGCCCTAAGGCCATIGCGTGCTGTCTAAATGGGAGGGTATGAAAGTTGTCGTG AAIGCGCTGGTTCAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTCTGATATTT GATGGTAATGACACTGTGCTGAGCCATGAAATCATACCGAATCGTAATGCCTGCAAAAGT TCACGAGAGGTGGACAAGCAGCCGATCCGAGAAACCAATATCTACATGTATTTATATTTC

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6318
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MEDIUM TYPE: Floppy disk
COMPOTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/608,618
                                                                                                                                                                                            T 12
US-08-608-618-2 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                  Sequence 2, Application US/08608618 Sequence 2, Application US/08608618 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Tinian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 196
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TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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SEQUENCE 6318 BP; 1713 A; 1349
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84.7%;
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                  4689 GTATICITCATCATATITGGATCCTITITCACACTCAATCTGTTCATTGGTGTTATCATT
                                     GATAATTTTAATGAACAAAAGAAGAAAGCAGGTGGATCATTAGAAATGTTCATGACAGAA
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APPLICANT: Soderlund, David M.
APPLICANT: Soderlund, David M.
APPLICANT: Knipple, Douglas C.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
TITLE OF INVENTION: HOUSE FLIES
CORRESPONDENCE: 19
CORRESPONDENCE: 19 21; 5948 5844 6008 5845 GGTGAAATTGGTGAGATAGCGGCGCGGACCGGACGCGAGGGATATGATCCGGTGTCGTCG 5904 2960 5829 TACAAGATCATACGATGGACATACCCATCTGTCGCGGGGACCTCATGTACTGCGTCGAC 5785 ATATIGGAIGCCCIGACCAAGGACTICITIGCGCGCAAGGGIAATCCGAICGAGGAGACG 5725 TACAAAATCATATCGATGGACATGCCGATATGTCGGGGCGACATGATGTACTGTGTGGGAT 84; C; 1592 G; 1664 T; 0 OTHER Indels 19603/600 (CRF D-1657) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: P.O. Box 1051, Clinton Square CITY: Rochester #1.30 0; Mismatches 814; Score 3660; DB 19; Pred. No. 0.00e+00; Version ВР

2343 2411 2247 2283 2351 GTATGGGACTGTTGTTGGGTGTGGTTAAAATTTCAGGAATGGGTCTCCTTTATTGTGTTC 2403 1766 1826 1827 1886 1887 1946 1947 2006 2007 2066 2067 2114 2127 2171 2187 2231 2291 1470 1530 1586 1590 1646 1647 1706 1707 1767 1410 GGCAAAATAAAACACCACGACAATCCTTTTATCGAGCCCGTCCAAACTCAAACAGTGGTA GGTCCCACATTCAAGGACATCGCCTCGAATATATCCTAAAAGGCATCGAAATCTTTTGT CGTGCTAGTGAACGAGGTG---------AGGACGATGACGAAGAT GAGAATGGTGCCATTATAGTACCAGCCTACTATTGTAATTTAGGTTCTAGACATTCTTCA TATACCTCGCATCAATAAATCTCGTATACATCACATGGTGATTTATTGGGTGGCATG GATGCCAATCACAAGGAACAAGGGATTATGAAATGGGTCAGGATTATACAGACGAAGCT GAACTGTTTGTTGGCGGCGAGAGGGCAACGATGACAACAACAAGAAGAAGATGTCGATA GATGCCCAGCAGTTTGCCCTATGCCGATGACTCGAATGCCGTAACACCAATGTCCGAA CGCAGCGTCGAAGTGGAATCGGAGTCGGTGAGCGTTATACAAAGACAACCAGCACCTACC 2248 2292 2284 2352 2344 2188 2232 1707 1947 2172 1647 1827 1828 1887 1888 1948 2007 2008 2067 2068 2128 1587 1591 1648 1708 1767 1768 1347 1411 1467 1471 1527 1531 1351 1407 1291 g g g ò g ð g ğ g g g δy ΩŸ Qγ Q δŽ g οy qq δ δλ ò g QY g Qγ g δŽ qq δý QQ QΥ g g δ ò

3492 P	3445 T	3552 T	3505 C	3612 0	3565 G	3672 G	3625 A	3732 A	3685	3792 Ċ	3745 G	3849 G	3805 I	3909 T	3865 A	3969 A	3925 G	4029 G	3985	4 089 A	4045 G	4149 G	4105 A	4 209 A	4165 C	4269 I	4225 A	4329 A	4285 I	4389 T	4345 G	4449 G	4405 G	4509 G	4465 T	4569 T
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QUENCE CHARACTERISTICS:
LENGTH: 1237 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Braman, Susan J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                            ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                      CCATGGAATTTATTTGATGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTCAGC
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                                                                            GATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAAACCATTAAAAAGCC
                                                                                                     ATTCCAAGACCGAGGTGGCGACCACAAGCAATAGTATTCGAAATAGTTACAGATAAAAAA
                                                                                                                                                        TACGACGCCTCCGAGGCGTACAACAATGTCCTCGACAAACTCAATGGGATATTCGTAGTT
                                                                                                                                                                                                                                    GACATCATTGAGAAGTATTTCGTATCGCCGACACTGCTCCGTGTGGTGAGAGTGGCCAAA
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                        5769 CAGCTGTCCGAATTCCTGGACGTACTCGGAGCCCCCGCTGCAGATCCACAAACCGAACAAG
                                                                                                                                                                                                                                                                                ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCGCAAGGGTAATCCGATCGAGGAGGACG
                                                                                  5665 CAGCTGTCCGAGTTCCTGGACGTGCTGGAGCCGCCGCTGCAGATCCACAAGCCGAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-808-793-26 STANDARD; DNA; UNC; 1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,361
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/08808793 Sequence 26, Application US/08808793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Soderlund, David M. APPLICANT: Soderlund, David J. TITLE OF INVENTION: CALCTUM PRITIE OF INVENTION: AND USE THUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34,103
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APPLICATION NUMBER: US 60/
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                          Length 1237;
                                         Score 472; DB 21; Length 12
Pred. No. 0.00e+00;
0; Mismatches 207; Indels
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE 1237 BP; 310 A; 309 C; 293 G; 325 T; 0 OTHER.
                                         Query Match 7.2%;
Best Local Similarity 76.6%;
Matches 679; Conservative
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T 14 US-09-024-020A-1 STANDARD; DNA; UNC; 5977

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RESULT ID US AC XX DT

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Sequence 1, Application US/09024020A

Sequence 1, Application US/09024020A

GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
SEQUENCE 5977 BP; 1478 A; 1554 C; 1600 G; 1345 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PACHOLIN RELEASE #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020A
FILING DATE: 16-FEB-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5977 base pairs
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                                                                                       GTCATCCTCTCCATTGTGGGAATGTTCCTGGCTGATATCATTGAGAAGTACTTCGTCTCC
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APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: FISH, LINDA M.
APPLICANT: SANGABESRARAN, LAKSHMI
APPLICANT: ASNORABESRARAN, LAKSHMI
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 4
ADDRESSE: JANET PAULINE CLARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
SEQUENCE 6007 BP; 1490 A; 1559 C; 1609 G; 1349 T; 0 OTHER.
                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC Compatible
OCRATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020A
FILLING DATE: 16-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 356; DB 23;
Pred. No. 0.00e+00;
                                                                                                                                                                                                     3401 HILLVIEW AVENUE, MS A2-250
JT 15
US-09-024-020A-2 STANDARD; DNA; UNC; 6007 BP.
                                                                                                                                                                                                                                                                                                                                                                                   CLASSILICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELEPHONE: (650) 852-3097
TELEPHONE: (650) 855-3307
TELEFAX: (650) 855-3322
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                Sequence 2, Application US/09024020A Sequence 2, Application US/09024020A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6007 base pairs
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Best Local Similarity 65.1%;
Matches 899; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                             CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
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                                                                                                                                                                                                           GGGATTGTCTTTGATTTCGTCACTCAACAAGCCTTTGACATTGTGATCATGATGCTCATC 4641
                                                                                                         4956 GGTCTGAACATGTTCACCATGACCCTCGATGGTTACGATGCGTCGGACACGTATAACGCG
                                                                                                                                                                                                                                                                                                                                          5242 AAAGGGGACTGTGGGAACCCCTCGGTGGGCATCTTCTTTTTTGTGAGCTACATCATCATC
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                                                                           5016 GTCCTAGACTATCTCAATGCGATATTCGTAGTTATTTTCAGTTCCGAATGTCTATTAAAA
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                     4522 AAAAAGCTGGGCTCCAAGAAGCCACAGAAGCCCATCCCCGACCCTTGAACAAAATCCAA
                                                                                                                                                                                              ATGTTTGCCTTGAGACACTACTATTTCACCATTGGCTGGAACATCTTTGACTTTGTGGTG
                                                                                                                                                                                                                                         GTCATCCTCTCCATTGTGGGAATGTTCCTGGCTGATATCATTGAGAAGTACTTCGTCTCC
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Db 5602 AA 5603 11 Oy 5907 AA 5908 Search completed: Sun Sep 13 08:58:55 1998 Job time : 5574 secs.

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16	308 4.7 6371 302 4.6 6342 296 4.5 6524 296 4.5 6524 296 4.5 6524 296 4.5 6527 296 4.5 6527 284 4.4 6373		RESULT 1 LOCUS 174672 6513 bp DNP DEFINITION Sequence 7 from patent US 5 ACCESSION 174672	S . Unknown. ISM Unknown. Unclassified. EL 1 (bases 1 to 6513) RS Arena,J.P., Feng,G., H. Wang,P. and Warmke,J.W.	TITLE Process for functional expr JOURNAL Patent: US 568917-A 7 18-N FEATURES Location/Qualifier Source 16513	T . 1681 a	Query Match 100.0%; Score Best Local Similarity 100.0%; Pred. Matches 6513; Conservative 0; N	Db 1 TCTAGACGTTGGCCGCATAGACAATGACA
######################################	>US-08-554-424-7 ption: (1-6513) from US t Score: 6513 I TCTAGACGT omp: AGATCTGCA g table: TABLE default	match STD : Dbase 0; Query 0	Searched: 532259 seqs, 918475165 bases x 2 Post-processing: Minimum Match 0% Listing first 45 summaries	Database: embl55 1:em_ba 2:em_htg 3:em_huml 4:em_hum2 5:em_in 6:em_om 7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro Database: genbank107 12:gb_ba 13:gb_htg 14:gb_in 15:gb_om 16:gb_ov 17:gb_pat 18:gb_ph 19:gb_pl 20:gb_pr1 21:gb_pr2 22:gb_ro 23:gb_st 24:gb_sts 25:gb_sy 26:gb_un 27:gb_v1	Mean 12.748	ater than or equal to the score of the result being pr rived by analysis of the total score distribution.	Result Query No. Score Match Length DB ID Description Pred. No.	13 1000.0 10 10 10 10 10 10 10 10 10 10 10 10 10 1

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6.73e-288

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Haematobia irritans pa Squid sodium channel m Mus musculus voltage-g Rat mRNA for brain sod Rattus norvegicus sodi Rattus norvegicus sodi Rat cardiac specific s Human voltage-gated softwar brown sapplens skeletal Rattus norvegicus mRNA for sod Rattus norvegicus mRNA Rat skeletal muscle vo Rattus norvegicus volt Aplysia californica so Rat brain mRNA for sod Rattus norvegicus volt Drosophila metanogaste Oryctolagus cuniculus Equus caballus skeleta H. saplens mRNA for volt Drosophila metanogaste Oryctolagus cuniculus Equus caballus skeleta H. saplens mRNA for volt Haematobia Irritans ex Rattus norvegicus sodi R. norvegicus mRNA for Sequence I from Patent Sequence 7 from Patent Sequence 5 from Patent M. musculus mRNA for Sn
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RESULT 1 LOCUS DEFINITION S ACCESSION NID REYWORDS	174672 6513 bp DNA Sequence 7 from patent US 5688917. 174672 93010813	PAT 23-DEC-1997	
SM	Unknown. Unknown.		
REFERENCE	onciassilitu. 1 (bases I to 6513) Arena,J.P., Feng,G., Hall,L.M., Liu,K., Van Der	Van Der Ploeg, L.H.T.,	
TITLE JOURNAL FEATURES	Wang, P. and Warmke, J. W. Process for functional expression of the Patent: US 568817-A 7 18-NOV-1997; Location/Qualifiers	the para cation channel	
SOLICE SASE COUNT ORIGIN	// // // // // // // // // // // // //		
Query Match Best Local Matches 65	Query Match Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 6513; Conservative 0; Mismatches 0;	Length 6513; ; Indels 0; Gaps	, ,
1	TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATAFCTGAGGAAGAAC	CGATATCTGAGGAAGAAC 60	
N 1 TC	TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC	CGATATCTGAGGAAGAAC 60	
3b 61 GC	GCAGTITGTTCCGTCCCTTTACCCGGGAATCATTGGTGCAAATCGAACAACGCATTGCCG	TCGAACAACGCATIGCCG 120	
2y 61 GC	GCAGTTTGTTCGTCCCTTTACCCGGGAATCATTGGTGGAAATCGAAATGATTGCTCC	TCGAACAACGCATTGCCG 120	
ob 121 CT	CTGAACATGAAAAGCAGAAGCTGGAAAGAAAGAGGCGGAGGGGAGGTGCCGGAT	AGGGAGAGGTGCCGCGAT 180	
λγ 121 CT	CTGAACATGAAAAGCAGAAGGAGCTGGAAAGAAAGAAGAGCCGAGGGAGG	AGGGAGAGGTGCCGCGAT 180	
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) 2y 181 AT			

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· 원	301 TCCCGCCGGAATTGGCCTCC	ACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 3	٠
οy	301 TCCCGCCGGAATTGGCCTCC	ACTCCTCTCGAGGATATCGATCCCTACTACAGCAATGTAC 3	ø.
QQ	361 TGACATTCGTAGTTGTAAGC	AAAGGAAAAGATATTTTGGCTTTTCTGCATCAAAAGCAA 4	OI C
δy	361 IGACATICGIAGTIGIAAGC	AAAGGAAAAGATATTTTCGCTTTTCTGCATCAAAGCAA 4	· 1
9 9 8	b 421 TGTGGATGCTCGATCCATTC.	AATCCGATACGTCGTGGCCATTTACATTCTAGTGCATC 4	08:
g	481 CATTATTTCCCTATTCAT	CATCACCACAATICTCGTCAACTGCATCCTGATGATAATGC 54	4
δ	481 CATTATTTTCCCTATTCAT	CACCACAATTCTCGTCAACTGCATCCTGATGATAATGC 5	4
qo e	541 CGACAACGCCCACGGTTGAG	TCCACTGAGGTGATATTCACCGGAATCTACACATTTGAAT 6	000
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a ž	601 CAGCTGTTAAAGTGATGGC		ف
Q	661 CATGGAATTGGCTGGACTT	CGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATT 7:	Ö
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g	781 TTGTGCCAGGCTTGAAGAC	CATCGTCGCGCCGTCATCGAATCGGTGAAGAATCTGCGCG 6	4
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q	841 ATGTGATTATCCTGACCAT	STRUCCCUGICGCIGITCCCCGTICATCGCCTACAGAICT	Ō
ογ	841 ATGTGATTATCCTGACCAT	STTCTCCCTGTCGCTTCGCGTTGATGGGCCTACAGATCT	Ō
Q	901 ATAIGGCGGGCTCCTCACCG	AGAAGTGCATCAAGAAGTTCCCGCTGGACGGTTCCTGGGGCA 9	Ψ.
γ̈́ο	901 ATATGGGCGTGCTCACCG	STGCATCAAGAAGTTCCCGCTGGACGGTTCCTGGGGCA	0
q	961 ATCTGACCGACGAGAACT	GGGACTATCACAATGCAATAGCTCCAATTGGTATTCCGAGG 1	7
δy	961 ATCTGACCGACGAGAACT	SACTATCACAATCGCAATAGCTCCAATTGGTATTCCGAG	
g	102	GTTATGCGGCAATATATCCGGTGCGGGGCAATGCGACGACG	80
οy	1021 ACGAGGCCATCTCATTTC	GTTATGCGGCAATATATCCGGTGCGGGGCAATGCGACGACG	8
g G	Db 1081 ATTACGTGTGCCTGCAGG	GTTTGGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT	14
Qγ	1081 ATTACGTGTGCCTGCAGG	GTTTGGTCCGAATCCGAATTATGGCTACACCAGCTTCGATT	4
Q	Db 1141 CGTTCGGATGGGCTTTCCT	GTCCGCCTTCCGGCTGATGACACAGGACTTCTGGGAGGATC	20
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<u>ස</u>	Db 1201 IGTACCAGCTGGIGITGCG	CGCCGCCGGACCATGCCATGCTTTTTATATATCATCA 	1260 1260
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S Arena, J. P., Feng, G., Hall, L.M., Liu, K., Var Wang, P. and Warmke, J. W.

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AAL Patent: US 5593864-A 7 14-JAN-1997;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. 58, 1143-1154 (1989)] kindly submitted by B.Ganetzky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophija melanogaster
Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Eracheata: Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 6883)
Loughney, K., Kreber, R. and Ganetzky, B.
Molecular analysis of the para locus; a sodium channel gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DROSODCHA 6883 bp mRNA INV 28-SEP-1993
Drosophila melanogaster para locus, sodium channel alpha subunit
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                                                                                               6240
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6241 AGAGTAATGTAAATAGTCCGGGTGAGGATGCAGCGGCGGCGGCAGCAGCAGCAGCAGCAGCAG
                                                                                                                                             CGGCGGCGGCGCGCGCGCGCGGGAAGTCCCGGAGCGGGTAGCGCCGGGCGACAGA
                                                                                                                                                                                                           CCGCCGTTCTCGTGGAGGGGACGGGTTCGTGACGAAGAACGGCCACAAGGTGGTCATCC
                                                                                                                                                                                                                                                                         CGCCCGCTGGTGGAGATGGTAGTGTTAACGGTACTGCAGAAGGAGCTGCCGATGCCGATG
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89184571
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/db_xref="taxon:7227"
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/db_xref="FlyBase:FBgn0003036"
                                                                                                                                                                                                                                                                                                                                                                                     CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA 6513
                                                                                                                                                                                                                                                                                                                                                                                                                   6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA 6513
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1. .6883
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M32078 M24285 M32079 M32080
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....6883
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/gene="para"
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Cell 58, 1143-1154 (1989)
89376565
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25-APR-1989
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AUTHORS
TITLE
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TITLE
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REFERENCE
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KGIKEQTQLEVAIGOGMEFTIHGDMKNNKPKKSKYLNNATDDDTASINSYGSHKNRPF
KDSBHKGSAFTWGGERKNDASKEDCLDELDEGEGEGEGEGEGDGDITHAHDEDILDE
YPADCCPDSYYKKFFTLAGDDDSPFWGGWGNRLKTFRIEDKYFTATHAHDEDILDE
ALALEDVHLPQRFILGDDILYYMDRIFTVIFFLEMLIKWLALGFKYYLTNAWCHDFYJ
WYSILNFWASLVGAGGIGARKTWRTLRALRPLAMSRWGGNRYVVNALVQALPSIFN
VLLVCLIFWLIFALMYQVGLFGKFKCEDMWGTKLSHEIIPNRACESENYTWNNSAM
NFDHVGNAYLLLFALWYQVGFRGKYRKCEDMWGTKLSHEIIPNRACESENYTWNNSAM
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SISPPLCGANTGSAGQCDDDVCLQGFGPPRYGYTSFDSFGARELSAFRLMTQDFWED
LYGLVLRAAGPWHMEFIVIIFLGSFYLVNLILAINAYDELQRKAEEEEAEEEA
REAEEAAARAAKLERRANAQAQAAADAAAAEBAALHPEMAKSPTYSCISYELFYGGE
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RKGSRSSHKYIIRNGRGRFGIPGSDRFVLVLSTYQDAQOHLPYADDSNAYTPMSEENG
ALIVPVYGGNLGSRHSYTSHOSRISYTSHGDLAGWANGVWGYGTMTKESKLRNNTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GISFPLCGNISGAGOCDDDYVCLQGFGPNPNYGYTSFDSFGWAFLSAFRLMTQDFWED
LYQLVLRAAGPWHMLFFIVIIFLGSFYLVNLILAIVAMSYDELQRKAEEEEAAEEBAI
REAEEAAAKAAKLEERANAQAQAAADAAAAEEAALHPEMAKSPTYSCISYELFVGGE
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VMVLNDIIEQAAGRHSRASDRGVSVYYFPTEDDDEDGPTFKDKALEVILKGIDVFCVW
DCCWVWLKFQEWVSLIVFDPFVELFITLCIVVNTMFMAMDHHDMNKEMERVLKSGNYF
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HKRPEPGDLDEDFRWFTDFMHSFWIVFRVLCGFWIESMMCWYGDVSGIPFELATVYI
GNIVVRIFFALLLSWFGSSSLSAFTADNDTNRTABAFNRIGRFKSWYRRIADCFKL
IRNKLTNQISDOPSGERTNQISWIWSEGKGVCRCISABHGDNELELGHBEILADGLIK
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RPQAIVFEIVYDKKEDIINMLFIGLNMFTMTLDRYDASDTYNAVLDYLNAIFVVIFSS
ECLKIRFARKHYFIEPWNLEDVYVYLLSILGIVLSDIIEKYEYSPTLLKVYRYKVĞ
RVLEVKGAKGIILLELAMSLPATNICLLLELVMFIFATEGMSFFMHYKEKSGIN
DVYNFKTEGQMILLEPQMSTSAGMDGYLDAIINEEACDPPDNDKGYPGKGSATVGIT
FLLSYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDDYDMYYEIWQOFDPEGTQY
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VMYLNDIIEQAAGRHSRASDRGEDDDEDGPTFKDKALEYILKGIDYFCVWDCCWWWLK
                                                                                                                                                                                                                                                                                                    /product-"sodium channel alpha subunit"

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/db_xref="PID:9403444"

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RAEGEVPRYGKRKKKGKERKDDEDEDEGPOPDFTLEGGVPIPVRLOGSFPPELASTPL
EDIDPYYSNVLTFVVVSKGKDIFRFSASKAMMALDPFNPIRRVAIYILVHPLFSLFII
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FVVIALAYVTMGIDLGNLAALRTFRVLRALKTVAIVPGLKTIVGAVIESVKNLRDVII
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RRGSRSSHKYTIRNGRGRFGIPGSDRKPLVLSTYQDAQQHLPYADDSNAVTPMSEENG
AIIVPVYYGNLGSRHSSYTSHQSRISYTSHGDLLGGMAVMGVSTMTKESKLRNRNTRN
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AAAAAAAAAAAACTTTAGSPGAGSAGRQTAVLVESDGFVTKNGHKVVIHSRSPSITSRT
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FVVIALAYVTMGIDLGNLAALRTFRVLRALKTVAIVPGLKTIVGAVIESVKNLRDVII
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ATMKLMAMSPRYYFQEGWNIFDFIIVALSLLELGLEGYQGLSVLRSFRLLRVFKLAKS
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PSGERTNQISWIWSEGKGVCRCISAEHGDNELELGHDEILADGLIKKGIKEQTQLEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTMFSLSVFALMGLQIYMGVLTEKCIKKFPLDGSWGNLTDENWDYHNRNSSNWYSEDE
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/translation="MTEDSDSISEEERSLFRPFTRESLVQIEQRIAAEHEKQKELERK
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EGEEKRDASKEDLGLDEELDEEGECEEGPLDGDIIHAHDEDILDEYPADCCPDSYYK
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                                                                                               /note="alternative exon d. All para mRNAs contain either alternative exon c (see variation) or alternative exon d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="alternative exon b for optional inclusion in mRNA"
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.3010,3173. .6667)
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EVA LAMATYTWG IDLGAULAGENETRY LIAGALETY AL PAGISTI 1048 TESWINKUNVI I ITMESLSYFALMGLOIYMGVATERCITEKT PLAGSAGNILTDENMOYHNRASSINWYSEDE GISFPLCGNISGAGQCDDDVCLQGFGPNPWYGTTSFDSFGWAFLSAFRLATQDFWED GISFPLCGNISGAGQCDDDVCLQGFGPNPWYGTTSFDSFGWAFLSAFRLATQDFWED LYQULLAAGAPHMEFPTVIFFGSFTLWILLAYVANASYDELQRAKEBEEBAEBEA I ERGERAAARAAKLEREANAQAAAAABEBAALHPERAKSDFTYSCISTELPGGFE RGADDNNKERMSITSVYSTESESSYSYLORQPAPTTAHQATKVRKYSTTSLELPGSFFNI RRGAGSSHKYTIKNGRGKFFFTGSCRKFULLSTYODAGQHLAYADDSNAVTPRABEENG AI IVPYYGNIGSRHSYTYSTGGSRKPLYLSTYDDAGQHLAYADDSNAVTPRABEENG AI IVPYYGNIGSRHSYTYSTGGSRYYTYFTGDLACTHRONGSTRKRSPYTRINKESERRENG AI IVPYYGNIGSRHSYTYTYGGENETROLAGACHTRONGSTRUKESERRENG AI IVPYYGNIGSRHSYTYTYGGENETRYLATACATHRONGSTRUKESPELFTROLAGANASPRYNTROLAGANASPRYNTRAMADHHANNE FTATFALBATMKLAMASPKYTPGGWNIFDFILVALSITERAWADHHANNEKEMERYLKSGNYFF FTATFALBATMKLAMASPKYTPGGWNIFDFILVALSITERAWADHHANNEKEMERYLKSGNYFF FTATFALBATMKLAMASPKYTPGGWNIFDFILVALSITERAWADHHANNEKEMERYLKSGNYFF FTATFALBATMKLAMASPKYTPGGWNIFDFILVALSITERAKSMPTLALLSSNGSSAPTADNOTNKIABAFNRIGRESWAVRNIADCFKLIRNY VLINLETAALLSNRGSSSAPTADNOTNKIABAFNRIGRESWAVRNIADCFKLIRNY VLINLETAALLSNRGSSAPTADNOTNKIABAFNRIGRESWAVRNIADCFKLIRNY VLINLETAALLSNRGSSAPTADNOTNKIABAFNRIGRESWAVRNIADCFKLIRNY VLINLETAALVATVIALLSSSSAAPTADNOTNKIABAFNRIGRESWAVRNIADCFKLIRNY CHINGSTRACHT COLFONTAGNKNNRGSKOVRGTSABANDON VANLINNACMLDEVINGTKATK LENDKOTNATALDEN THANDEDLILDEYPE DE THANDEDLILK KEK KENTINNACWILDEY VANLINGT CHINGSTRACHT KACH KENTERLEN TINNETATULIV VCINKALTEN NACHOLOGNATVATUL NAVLINGT KENTER LIEGADDSPROGNATVANALVQA I PSITRULV VCINKALTEN TROLAGANATHLANGSKRYTSABANTON VON THAN AT THE LIEGANT TROLAGANATHLANGSKRYTTAL LAGASTALA TRUKCAGAGTALA TRUKCAGAGTALA TRUKCAGAGTALAN TRULLAGAGTAN TRULLAGAGTA TRUKCAGAGTA TRUKCAGATA TANTATALANGSTALA TATATANGSTATAL TATATANGSTATALANGSTANATALAGAGTA TATATATANGSTATAL TATATATANGSTATALANGSTANATALAGAGTA TATATATANGSTATALANGSTANATALAGAGTA TATATATANGSTATALANGSTANATALAGAGTA TATAT /codon_ftart=1
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Query Match 1035 855 915 299 975 727 675 735 487 Matches 247 555 307 615 367 375 127 495 255 7 315 67 435 187 g δý g ò g ŏ ò g g ò g QΥ g δ g Qγ g δ g ö g Q g ò g ò ά /product="sodium channel alpha subunit"
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annotations omitted

Note: remainder of

CDS

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CGGATCCTACACTTGAACAGGTGTGCCAATACCTGTTCGATTGCAGGGGAGCTTCCGGC 554
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTCGATCCATTCCAATCCGATACGTCGTGGGCCATTTACATTCTAGTGCATCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTAAAGTGATGGCACGAGGTTTCATTTTATGCCCGTTTACGTATCTTAGAGATGCATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGGCTGGACTTCGTAGTAATAGCTTTAGCTTATGTGACCATGGGTATAGATTTAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAACGCAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTAGTTGTAAGCAAAAGGAAAAGATATTTTCGCTTTTCTGCATCAAAAGCAATGTGGA
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Score 5992; DB 14; Length 6883;
Pred. No. 0.00e+00;
0; Mismatches 97; Indels 45;
   92.0%; S.larity 97.8%; F.Conservative
                   Local Similarity
nes 6359; Conserv
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	TAT	Ä	GCGT(CGA	CCGA	GCAT((7)	- GT-	ATG	GATG	AGCTO 1111 AGCTO	ÿ	AGG.	ည် <u>-</u>	- Æ	AAGC	- 7 1	CAGC	S S	CGTA CGTA	₹ S	ACAAA(AAAGA(AAAG	ATC =	- ()	AGTACAC	AGTA	TGGTZ	GGT	CCGT
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	qq	οy	q ò	g 2	φy	da Qy	qq	Οy	g	δ	g &	· 6	δ	g	δy	qq	δŏ	යි :	Š	g &	· 음	οy	QQ	δ	QQ	ογ	gg	ογ	ф	δλ	දු දු

qq	2175	AGGCTCCCGACACTCATCGTATACCTCGCATCAGTCCCGAATATCGTATACCTCACATG 223
ογ	1927	
qq	2235	CGTCATGGGCGTCAGCACAATGACCAAGGAGAAT 229
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අු	2295	TGCGCAACGCAACACGCAATCAATCAGTGGGCGCCACCAATGGCGGCACCACCTGTC 2354
δλ	2047	GCGCAACCGCAACACCAATCAATCAGTGGGCGCCACCAATGGCGGCACCACTGTC 210
g	2355	
οy	2107	GGACACCAATCACAAGCTCGATCATCGCGACTACGAAATTGGCCTGGAGTGCACGGACG 216
පි	2415	TTTTATCGAGCCCGTCCAGACACAAACGG
δλ	2167	SCTGGCAAGATTAAACATCATGACAATCCTTTTATCGAGCCCGTCCAGACACAAACGG
ති	2475	CGCTGGTCGGC
δλ	2227	GGTIGATATGAAAGATGTGGTGTCCTGAATGACATCGAACAGGCCGCTGGTCGGC
đ	2535	TTACTATTTCCCAACAGAGGACGATGACG
δλ	2287	AGTCGGGCAAGCGATCGCGGTGTCTCTTTACTATTTCCCAACAGAGGACGATGACG
d G	2595	AGGATGGGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGTGT 2654
QY	2347	SATGGGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCGATGTGT
g G	2655	TGTGTGGGACTGTTGCTGGGTTTGGTTGAAATTTCAGGAGTGGGTATCGCTCATCG
δλ	2407	TIGTGTGTGGGACTGTTGCTGGGTTGGGTTGAAATTTCAGGAGTGGGTATCGCTCATCG
Q	2715	TICGAICCCITCGICGAGCICTICAICACGCIGIGCAITGIGGICAACACGAIGIICA
οy	2467	CTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGTGCCATTGTGGTCAACACGATGTTCA
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Οy	2587	ITCITCACGCCACCTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGAGCCCA
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5309 5429 5046 5106 5369 5226 5189 4986 4386 4649 4446 4709 4769 4829 4889 4686 4746 5009 4806 5069 4866 5129 4469 4266 GAATATTTACGGTTATATTCTTCTTGGAAATGTTAATCAAGTGGTTGGCGCTCGGCTTCA 4146 GCGATATTATCGAGAAGTACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGCGTGTGGCGA AATTCGATATAATCATTATGTTATTCATTGGTCTGAACATGTTCACCATGACCCTCGATC AGCCATGGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTTA CCATTCCAAGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGA ATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATTTATATT AAGTGTACTTGACCAACGCGTGGTGTTGGCTCGATTTCGTGATTGTCATGGTATCGCTTA GCGAGAACTACACGTGGGTGAATTCAGCAATGAATTTCGATCATGTAGGTAACGCGTATC CGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCAGGGCATGAGGGTCGTCG TTAATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGTCTAATAT TTTGGCTAATTTTTGCCATAATGGGTGTACAGCTTTTTGCTGGAAAATATTTTAAGTGCG AGGACATGAATGGCACGAAGCTCAGCCACGAGATCATACCAAATCGCAATGCCTGCGAGA 5250 5047 5310 5370 4867 4927 5107 5167 5010 5070 5130 5190 4987 4590 4650 4447 4710 4507 4770 4567 4830 4627 4890 4687 4950 4747 4807 4207 4470 4267 4530 4327 4387 4350 4147 4410 4087 g g g g δŽ qq δλ ద δy g QY В δy 셤 Ω QΩ QΥ g δy ٥y ò g οy QΥ g P Q δy g g ŏ g Q à g ά δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ., Doyle, K.E., Marsella-Herrick, P.A. and Soderlund, D.M. ic linkage between the kdr insecticide resistance trait ge-sensitive sodium channel gene in the house fly Acad. Sci. U.S.A. 91 (7), 2483-2487 (1994)
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15-JAN-1997) Dave M. Soderlund, Entomology, New York
ultural Experiment Station, Cornell University, Castle
leva, W1 14456, USA
and protein update by submitter
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-1995) Dave M. Soderlund, Entomology, New York ultural Experiment Station, Cornell University, Castle eva, NY 14456, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams, P.M., Knipple, D.C. and Soderlund, D.M. ation of voltage-sensitive sodium channel gene coding rom insecticide-susceptible and knockdown-resistant trains hem. Mol. Biol. 26 (4), 319-326 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6318 bp mRNA INV 19-FEB-1997 tica insecticide-susceptible strain voltage-sensitive nel mRNA, complete cds.
                                                                                                                                                                                                                            6899
                                                                                                                                                                  6426
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mitochondrial eukaryotes; Metazoa; Arthropoda;
Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
; Muscoidea; Muscidae; Musca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams, P.M., Knipple, D.C. and Soderlund, D.M.
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COUNT BASE CO

21; 570 510 626 989 326 390 446 450 506 Gaps ACTATICTAACTAATTGTATTTTAATGATAATGCCGACAACGCCCACGGTCGAATCCACA ATAGCTTTAGCTTATGTGACCATGGGCATAGATTTAGGTAATCTCGCAGCTTTGAGAACA ATACGATATGATGACGAGGACGAAGATGAAGGTCCACAGCCGGATCCCACACTTGAACAG ATCCGATATGATGACGAGGACGAGGATGAAGGTCCACAACCGGATCCTACACTTGAACAG **AAGGATATTTTTCGTTTTTCTGCCTCAAAAGCAATGTGGCTGCTCGATCCATTCAATCCG ACAATTCTCGTCAACTGCATCCTGATGATAATGCCGACAACGCCCACGGTTGAGTCCACT** GAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTGATGGCACGAGGT TTCATTTTATGCCCGTTTACGTATCTTAGAGATGCATGGAATTGGCTGGACTTCGTAGTA GGTGTGCCTATACCTGTTCGAATGCAGGGCAGCTTCCCGCCGGAATTGGCCTCCACTCCT CTCGAGGATATCGATCCCTTCTACAGTAATGTACTGACATTTGTAGTAATAAGGA ATACGTCGTGTAGCCATTTATATTTTAGTGCATCCCTTGTTTTCGTTATTCATCACC 84; Length 6318, Indels score 3676; DB 14; pred. No. 0.00e+00; 0; Mismatches 806; Score Pred. 1 tch 56.4%; al Similarity 84.9%; 4986; Conservative Query Match Best Local (tches 571 151 207 211 267 271 327 331 387 391 447 451 507 511 267 627 631 687 ద 셤 à 셤 ò 셤 ö g õ 셤 ò ద ç 셤 ő ò d ç

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7 A			qq	2944
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g	2068	GATGCCAATCACAAGGAACAAAGGGATTATGAAATGGGTCAGGATTATACAGACGT 2127	QQ	3124
\ 6			ΟŊ	3192
· E	2128	GGCABABATABABACACACCACAACABCATTATTTATTTATT	qq	3184
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· 6		GACATGAAAGATGTTATGGTCTTAAATGATATGAACAAGCCGCTGGTCGGCATAGT 2247	තු	3244
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ţ			Qγ	3968

TCAATAAACCACCAAGACAATAGACTGGAACATGAGCTAAACCATAGAGGTTTGTCCATA 3504 2 ATGGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCTTTCCGGATGGC 2951 GAACTGGAGCTGGGCCACGACGACGACGGCCTCATCAAGAAGGGATCAAG CTGGATGGTGACATTATCATTCATGCGCAAAACGACGACGAGATAATCGACGACTATCCG AATATTGCCGATTGTTTAAGTTAATTCGAAATAAATTGACAAATCAAATAAGTGACCAA AAAGAGGACCTCGGCCTCGACGAGGAACTGGACGAGGAGGCCGAGGGCGATGAGGGCCAG GCTTTGCTTTTGTCCAACTTCGGTTCATCTAGTTTATCAGCCCCGACTGCCAATGAT CCATCAG------A-A-CA-----TGG--CGAT-A--ATG-----CCATCAGGTGAGAGGACCAACCAGATCAGTTGGATTTTGGAGCGAAGAGCATGGTGACAAC -AACTGGAGTTGGGTCATGACGAAATCATGGGCGATGGCTTGATCAAAAGGGTATGAAG GGCGAGACCCCAGCTGGAGGTGGCCATTGGCGATGGCATTCACGATACATGGCGAT **ATGAAAAACAACAAGCCGAAGAAATCAAAATTCATGAACAACACAACACGATGATTGGAAAC** CAGGACGATGACACTGCCAGCATTAACTCATATGGTAGCCATAAGAATCGACCATTCAAG AAATATTTTGAAACCGCAGTTATCACTATGATTTTAATGAGTAGCTTAGCCTTTGGCCTTA GAATTACCGCCGCTGGAACTTCACCGACTTCATGCACACCTTCATGATTGTGTTCCGAGTG ACCAATAAAATAGCAGAGGCCTTCAATCGTATTGCTCGTTTTAAGAACTGGGTGAAACGT ~ Ċ, Ŋ ß

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5168 5288 5348 5408 5468 5528 5184 5244 5304 5364 5424 5484 5588 5544 5648 5708 5604 5664 5768 5724 5828 5844 5948 6008 $\begin{array}{ccc} \text{RNA} & \text{INV} & 17\text{-SEP-1996} \\ \text{voltage-sensitive sodium channel, complete} \end{array}$ 5784 5888 GGTGAAATTGGTGAGATAGCGGCGCGCGACCGGACACCGAGGGCTATGATCCGGTGTCGTCA 5904 5960 6064 GACATCATTGAGAAGTATTTCGTATCGCCGACACTGCTCCGTGTGGTGAGAGTGGCCAAA CAGCTGTCCGAGTTTCTGGACGTGCTGGAGCCGCCGCTGCAGATCCACAAGCCGAACAAG GTGGGTCGTGTCCTGCGTTTAGTCAAGGGTGCCAAGGGTATCCGGACGTTGCTGTTCGCG TTAGCCATGTCGTTGCCTTATTCAACATTTGTCTGTTGCTGTTCTTGGTGATGTTC TCAGCCGGTTGGGATGGTGTTAGATGCCATTATCAATGAGGAAGATTGCGATCCACCC GACAACGACAAGGGCTATCCGGGCAATTGTGGTTCAGCGACTGTTGGAATTACGTTTCTC CITICATATCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTGTCATTCTC GAGAACTATAGCCAGGCTACGGAGGATGTACAGGAGGTCTCACCGACGACGATTACGAT ATGTACTACGAGATTTGGCAACAATTCGATCCGGAGGGCACCCAGTACATACGCTACGAC ATATTGGATGCCCTGACCAAGGACTTCTTTGCGCGCAAGGGTAATCCGATCGAGGAGACG ACACTGTGGCGCCCAGCGTGAGGAGTACTGCGCCAAGCTGATACAGAATGCGTGGCG CDS. X96668 91550780 voltage-sensitive sodium channel. house fly. MDPARA 6899 bp M.domestica mRNA for RESULT 6 LOCUS DEFINITION φ 5409 5605 5065 5125 5185 5305 5469 5905 5169 5229 5365 5425 5529 5485 5589 5545 5649 5709 5665 5769 5725 5829 5785 5889 5845 5949 6009 ACCESSION NID KEYWORDS SOURCE 유 δ qq δ g δy g ò g δý g ò g ò g δ g g g q à δy δy ò 셤 δ g ò g δy a ò

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QMSTSAGWDGVLDAIINEEDCDPPDNDKGYPGNCGSATVGITFLLSYLVISFLIVINM
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                                                                                tazoa; Arthropoda;
Diptera; Brachycera;
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Submitted (15-MAR-1996) M.S. Williamson, IACR-Rothamsted,
Department of Biological & Ecological Chemistry, Harpenden,
Hertfordshire, ALS 230, UK
Location/Qualifiers
1. .6899
/organism="Musca domestica"
//incompage: //inco
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Williamson,M.S., Martinez-Torres,D., Hick,C.A. and Devonshi
Identification of mutations in the housefly para-type sodii
channel gene associated with knockdown resistance (kdr) to
                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa;
Iracheata; Hexapoda; Insecta; Pterygota; Dipter
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/note="alpha subunit"
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14. .6340
                                                                        Sukaryotae; mitochondrial
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DB 14; Length 6899;

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                           ATACGATATGATGACGAGGACGAAGATGAAGGTCCACAGGCCGGATCCCACACTTGAACAG 223
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Direct Submission
Submitted (15-JAN-1997) Dave M. Soderlund, Entomology, New York
State Agricultural Experiment Station, Cornell University, Castle
Strate, Geneva, NY 1456, USA
Nucleotide and protein update by submitter
Location/Qualifiers
1. .6315
/organism="Musca domestica"
/strain="Kdr"
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Direct Submission
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/note="insecticide-resistant reference strain"
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Pred. No. 0.00e+00;
0; Mismatches 812; Indels 84;
                                                                                                                                                                                                      /product="voltage-sensitive sodium channel"
                                      /db_xref="taxon:7370'
                                                                             /chromosome="3'
                                                                                                                                                                    /codon_start=1
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2644 TIGGGCCTGGAGGGTGTCCAGGGCCTGTTGAGAAGTTTTGGTTTGCTTGC	ΟŸ	3792
	qa	3745
2704 TICAAATTGGCAAAATCATGGCCCACACTGAATTTACTCATTTCAATTATGGCACCGAAA 2703 111111 1111	Qy	3849
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2764 AIGGGIGCATIGGGTAAICTGACATITGTACTITGCATTATCATCTTTGCATG 2823 	QY	3906
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	Qy	3968
GAATTACCGCCTGGAATTTCACCGACTTCATGCACGTTCATGATTGTGTTGTTTCCGAGTG	<u>අ</u>	392
	δ.	4029
2944 CIGIGCGGAGAGIGGATCCAGTGTGGGACTGCATGTATGTGGGCGATGTCAGGTGT 3003	g :	865
3012 CICTGCGGAGAATGGATCGAGTCCATGTGGGATGTACGTGGGCGGTGTTCTCGTGC 3071	Š É	* 5
4 ATACCCITCITCITGCCACGGTCGTGATCGGCAATTTGTGGTTCTTAATCTTTA 306	8 8	4149
313	qa	410
3064 GCTTTGCTTTTGTCCAACTTCGGTTCATTTATCAGCCCCGACTGCCGACAATGAT 3123 113 GCTTGCTTTTGTCCAACTTTGGCTCATCTTATCAGCGCCGACTGCCCGATAAGAT 111 11	δδ	420
ACCAATAAATAGCAGAGGCCTTCAATCGTATTGCTCGTTTTAAGAACTGGGTGAAACGT 31	셤	416
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3555 GALGARAGCCALARGGCLACCARGACLATICARGGCCARGAGAGAGAGAGAGCGCGAGC 3624 [QY	
25 PACING CONTROLL CONTROL CON	d d	470
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 ATTCCAAGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCGATAAGAAA
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                       TTCGATATAATCATTATGTTGTTCATTGGCTTAAACATGTTTACCATGACCCTCGATCGG
                                  TACGACGCCTCCGAGGCGTACAACAATGTCCTCGACAAACTCAATGGGATATTCGTAGTT
                                                                                           4989 TACGAIGCGICGGACACGIATAACGCGGICCIAGACIAICICAAIGCGAIAIICGIAGII
                                                                                                                                                                 CCATGGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTGTACTCAGC
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Kranslation-"MSDDSSSISEERSLFRPFTRESLAAIEARIAEEYAKQKELEKK
RAEGEWYRUDEDEDEGEGPOPDALLEGGAAIPYRMOGIEPPELASTPLEDIDPFYHNORT
FVVVSKGKDIFRFSATDAMWILDPFNPIRRVAIYILVHPLFSLFIITTILTNCIFMIM
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DKORNDSEIGCYFGDGGSATVGTAFLGYLVIESTLIVIMYTAVLLENYSQATEDVORG
LTDDDVDMYYEIWQGFDPGGTGATYGTREYDGLSPFLDVLEPPLQIHKPNKYKIVSMDIPIC
KGDLMFCVDILDALKDFFARKGNPIESSAELGEVQPGRPDEVGYFEPVSSTLMRQRER
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IDLGNLAALRTFRVLRALKTVAIVPGLKTIVGAVIESVKNLRDVIILTMFSLSVFALM
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Tracheata, Hexapoda, Insecta, Pterygota, Orthopteroidea, B
Blattellidae, Blattellinae, Blattella.
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/note="Pyrethroid insecticide-resistant strain"
/db_xref="taxon:6973"
                                  ACACTGTGGCGCCAGCGTGAGGAGTACTGCGCCAAGCTGATACAGAATGCGTGGCG
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Insect Biochem. Mol. Biol. 27 (2), 93-100 (1997)
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Lansing, MI 48824, USA
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                                               Score 1912; DB 14; Length 6096;
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                                                                                  5605 TAAGCTTTTGATAGTTATTAATATGTACATTGCTGTCATCTCGGGAACTATAGTCAGG
                                                                                                                                                      5725 GGCAGCAATTCGATCCGGAGGCACCCAGTACATACGCTATGATCAGCTGTCCGAATTCC
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                                                                5444 TCAGITTCCTTATTGTTATTAACATGTACATTGCTGTCATTTTGGAGAATTACTCCCAGG
                                                                                                                                   CGACAGAGGATGTGCAGGAAGGCTTGACGGATGATGACTACGATATGTACTATGAAATTT
                                                                                                                                                                                                   GGCAGCAGTTTGACCCAGATGGGACGCAATATATTCGCTATGACCAGCTGTCGGATTTCC
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Tracheata: Hexapoda; Insecta; Pterygota; Orthopteroidea; B
Blattellidae; Blattellinae; Blattella.
1 (bases 1 to 6096)
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/db_xref="taxon:6973"
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/organism="Blattella
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Lansing, MI 48824, USA
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29.3%;
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740 GGCCGCTTTGGTAT-ACCCGGTAGCGATCGTAAGCCATTGGTATTGTCAACATATCAG 747 GATGCACAAGAACATCTTCCTTATGCAGATGACTCGAATGCCAGTAACCATTGTCAAGAGC 11111 1 1 1 1 1 1 1 1	75 AA-CAACCTT 1 1 1 1 67 AATCAATCATT 19 G-TCAGCA-GA 1 1 1 1 27 GATCATCGGA 60 C-TGACAATCC 1 1 1 1 1 87 CATGACAATCC 19 ATGGTGCTGAA 19 ATGGTGCTGAA	79 GG 11 07 GG 36 GA 67 GA 67 GA 11 27 TG 11 16 17 18 17 18 17 18	16 ATGAATAAAGACATGGATAAGGCTCTCAAGAGTGGCAACTATTCTTCACAGGGACCTTT
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Š	7	AAIGGGIGIACAGTITITGCIGGAAAAIATTITAAGTGCGAGGACATGAATGGCACGA 440
අ දි	30	CTTTGAGCCACGAAATCATTCCTGACAGAAATGCTTGCATTGCTGAAAACTACACATGGG 436
Š	4	AGCICACCACGAGAICAIACCAAAICGCAAAIGCCIGCGAGAGCGAGAACIACACGIGGG 452
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9 Z	4484	AGCAGCCAAICCAGGAACGAAACGAACATCAACGTACCTTTGCGTTTGCTGTTCTTTGTGTT 4543
ద	4544	TIGGCTCATTITICACTCTCAACCTATTCATTGGTGTGATCATCGACAACTTTAATGAGC 4603
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g	4604	AAAAGAAAAGGCAGGAGGGTCGCTAGAGATGTTCATGACTGAAGATCAGAAGAAATACT 4663
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δ	4885	GGCGACCACAAGCAATAGTCTTTGAAATAGTAAGGAAATTCGATATAATCATTA 4944
g	4784	TGTTGTTCATTGGCTTTAACATGTTAACAATGACTCTGGATCACTATCAACAGTC
δγ	4945	TGTTATTCATTGGTCTGAACATGTTCACCATGACCCTCGATCGTTACGATGCGTCGGACA 5004
д	4844	AGTICAGCGACGTICTIGATIACTIGAACAIGATCTICATCGTCATCTTCAGTICCGAGT 4903
ò	5002	CG
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DVUZ6343 2144 bp mRNA INV 10-DEC-1995 Corsophila virilis sodium channel protein (para) mRNA, partial cds. UZ6343 91110461

LOCUS DEFINITION ACCESSION NID

KEYWORDS

FEATURES

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SYYEPTEDDDEDGPLKDRALEVILKGIDVPCVMCCWWHEKGEWSLIVEDPFVE
SFTILCIVVNTMFKAMDHHDNNKEMERVLKAGNYFFTFALEATFALEMKLAAAMSRYYYEO
EGWNIFDFIIVALSLLELGLEGVQGLSVLRSFRLLRVFKLAKSWPTLNLLISIMGRTM
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NKEMERVLKAGNYFFTATFALEATWKLAMASPKYFPOEWNIFDFITLCIVVTWFMAMDHHDM
NKEMERVLKAGNYFFTATFALEATWKLAMASPKYFPOEWNIFDFITLVALSILELGGLE
GVQGLSVLKRFRLLRYFRAKSWPTLNLLISINGRTMGALGNLTFVLCIIIFIFAVMG
MQLFGKNYHDHKDRFPDFDGLDFRWNFTDFMHSFMIVFRYLCGEWIESWMDCMYYGDVSC
IPFFLATVVIGNLVVLNLFLALLLSNFGSSSLSAPTADNDTNKIAEAFNRIGRFKSWY
KRNVAGCFKLIRNKLTNGLYGOSPSGERINOLSWIWSEGKGVCRCISAEHGDNELEGH
DEILADGLIKKGIKGJYQLEVAIGGOMFFTIHGDMKNNKFKKSKYLNNATWIGNSINH
QDNRLEHELNHRGLSLQDDDTASINSYGSHRNRFKERSKYLNNATWIGNSINH
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STEGLECTDDEAGKIKHDNPFIEDVQTQTVVDMADDVMLDDIEQAGAGNSKENSRASDRGV
SVYYEPTEDDDEAGKIKHDNPFIEDVQTQTVVDMADVMVLKFQGEWYGLIPDFVE
LFITLCIVVNTWFMAMDHHDMNKEMERVLKAGNYFTATFAIEATMKLMAMSPKYYFQ
EGWNIPDFITTYALSLLEGLEGVQGLESVARSFRIARPKTAKSNPTLMLISINGRYM
GALGNITFVLCIITFRAGAGRAGLEGVQGGENYHDHKDRFPDGDLPRWHTDFMHSFNIVFR
VLCGEWIESMWDCMYVGDVSCIPFFLATVVIGNLVVLNLFLALLLSNFGSSSLSAPTA
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RISYTSHGDLLGGMAVMGVSTWTKESKLRNRNTRNQSVGATNGGTTCLDTNHKVEHRD
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SDRKPLVLSTYQDAQQHLPYADDSNAVTPMSEENGALIVPVYYGNLGSRHSSYTSHQS
RISYTSHGDLLGGMAVMGVSTMTKESKLRNRNTRNQSVGATNGGTTCLDTNHKVEHRD
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SVYYEPTEDDDEDGPTLKDRALEVILKGIDVFCVWDCCWWWKRFQEWYSLIVEDPFVE
LEITLCIVVNYMFMAMDHHDMNKEMERVLKAGNYFFTATFATEATEATMKLMAMSPKYYFQ
EGWIFPFILVALSLIELGEGVQQLSYLRSFRLLKVFKLAKSWPTLNLLISINGRTM
GALGNITFVLCIIIFTEAVMCMQLFGKNYHDHKDRFPDGDLPRWFTDFMHSFYY
VLCGEWIESWMDCMYVGDVSCIPFFLATVVIGNLVVLNLFLALLLSNFGSSSLSAPTA
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GRODNELECHDELIAMOLIKKGIKEQTQLEYAIGDGREFTIHGDMKNNKPKKSKYLN
GHTMIGNSINHQDNNEHELNHKGLSLQDDDTASINSYGSHKNRPFKDESHKGSRETM
EGEEKRDASKEDLGLDEELDEE
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/translation="ATKVRKVSTTSLSLPGSPFNIRRGSRSSHKYTIRNGRGRFGIPG
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/db_xref="ptD:gl110464"
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SDRRPLYLSTYQDAQQHLPYADDSNAVTPMSEBNGAIIVPVYYGNLGSRHSSYTSHQS
                                                                                                                                                                                                                                                                                                                                   /product="sodium channel protein"
/db_xref="PID:gl110467"
/db_xref="PID:gl11047"
/db_xre
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                                                                                                                                                                                                           /note="lacking alternate segment a"/codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="sodium channel protein"
/db_xref="PID:g1110462"
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/note="lacking alternate segment
/codon_start=3
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                                                                                                                                            /standard_name="paralytic"
join(<1. .29,93. .>2144)
/gene="Dvir\para"
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/gene="Dvir\para"
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/db_xref="PID:g1110488"

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EGWNIFDFIIVALSLLELGLEGVQGLSVLRSFRLDHKDRFPDGDLPRWNFTDFWHSFM
IVFRVLCGEWIESMWDCMYVGDVSCIPFFLATVVIGNLVVLNLFLALLLSNFGSSSLS
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LETITLCIVWFWFWAMOHHDNIKEMERTLKAGNFFTARTAGATBATMKLAMSPRYYFO
EGWNIFDFIIVALSLLELGSLEGVOGLSVLRSFRLLRYFKLAKSWPTLALLISINGRYM
GALGNLTFVLCIIIFIFAVMGMQLFGKNYHDHKDRFPDGDLPRWNFTDFMHSFMIVFR
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DUDTHNITAEAFPRIGRPKSWKRNVADADOFKLIRNKLTNOLSDPGSGERINGISWWSE
GRGYCRCISABHGDMPELEKBDEILADGLIKKGIKEOTOLEVALGDOREFTIHGDMKN
NKPKKSKYLNNATDDDTASINSYGSHKNRPFKDESHKGSAETWEGEEKRDASKEDLGL
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SDRRPLVLSTYQDAQQHLPYADDSNAVTPMSBENGAIIVPVYYGNLGSRHSSYTSHQS
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IWSEGKGVCRCISAEHGDNELELGHDEILADGLIKKGIKEQTQLEVAIGDGMEFTIHG
DMKNNKPKKSKYLNNATMIGNSINHQDNRLEHELNHRGLSLQDDDTASINSYGSHKNR
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YEIGLECTDEAGKIKHHDNPFIEPVQTQTVVDMKDVMVLNDIIEQAAGRHSRASDRGV
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                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 2144)
Hackeray, J.R. and Ganetzky, B.
Conserved, alternative splicing patterns and splicing signals in the
Drosophila sodium channel gene para
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Thackeray,J.R. and Ganetzky,B.
Developmentally regulated alternative splicing generates a complex array of Drosophila para sodium channel isoforms
J. Neurosci. 14 (5 Pt 1), 2569-2578 (1994)

    .2144
    /organism="Drosophila virilis"
    /note="cDNA was derived by RT-PCR; sequence compiled from 6 independent clones"
    /db_xref="taxon:7244"
    /chromosome="x"

                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-MAY-1995) Justin R. Thackeray, Biology, Yale University, 266 Whitney Avenue, New Haven, CT 06520, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFKDESHKGSAETMEGEEKRDASKEDLGLDEELDEE
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/note="lacking alternate segment d"
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|join(<1. .1913,1989. .>2144)
/gene="Dvir\para"
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/gene="Dvir\para"
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Thackeray, J.R. and Ganetzky, B.
Direct Submission
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/gene="Dvir\para"
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                                                                                    Drosophila virilis.
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                                                           AAATGGAACGTGTGCTCAAGGCTGGCAACTATTTCTTCACCGCCACATTGCAATTGAGG
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                        CCATCATAGTGCCCGTGTACTATGGCAATCTAGGCTCCCGACACTCATCGTATACCTCGC
                                                                                                               TGGCCCCACAAATGGGGGCACCACCTGCCTGGACACCAATCATAAGGTCGAGCATCGGG
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VLGEWIESMMDCMYGDVSCIPFELATVYIGNLVVLIALFLALLLSNFGSSSLSAPTA
DNDTNKIABAFNRIGRFKSWKRNVADDCFKLIRNKINGISDQPSGKGVCRCISABHG
DNELELGHDEILADGLIKKGIKEGYOLGVGMEFTIHGDMKNNKFKSKYLNNAT
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                                                                                                                      /product-"sodium channel protein"
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Pred. No. 0.00e+00;
0; Mismatches 171;
                                                                                                    /note="lacking alternate segment
/codon_start=3
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                                                                 join(<1. .654,679. .>2144)
/gene="Dvir\para"
                                                                                        paralytic"
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/gene-"Dvir\para"
/note-"optional segment b"
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/gene="Dvir\para"
/note="optional segment
c in some cDNA's"
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/gene="Dvir\para"
/note="Optional segment
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Best Local Similarity 90.6%;
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Note: remainder
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DKKFDMIIMLFIGFNMLTMTLDHYQQSKQFSDVLDYLNMIFIVIFSSECLMKIFALRY
HYFKEPWNLFDFVVVILSILGLVLSDIIEKYFVSPTLLRVVRVAKVGRVLRLVKGAKĞ
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VAGGGIQAFKTWRTLRALRPLRAMSRNGGMRVVNALVQATBSIFVLLUVLLYWLIFWLI
FYRGKYYKCVDSNSTLSHEI IDPRNACIABNYTWRNSPMRDHVGRAYLC
LEQVAFEKGHTQIMNDAIDSRBLHKQPIRETNIYMYLYFVFFIIFGSFFTLNLFIGVI
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MILLFQMSTSAGWDGVLDGIMNEEDCNKPNSEIGYPGDCGSATVGIAFLLSYLVISFL
IVINNYIAVILLENYSQATEDVQEGLTDDDYDMYYEIWQOFDPDGTQYIRYDQLSDFLD
                                                                                                                                                                                                                                                                                                                                        /translation="AwnwldFvvIalayvTwGIDLGNLAALRTFRVLRALKTVAIVPG
LKTIVGAVIESVKNLRDVIILTMFSLSVLALMGLQIYMGVLTOKCIKNFPINGSWGEL
NDENWHAFCSNNTNWYFPEGAPEVPLCGNSSGAGTCPPVYTCLQGFGENPNYGYTSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="single amino acid change in protein compared to
KRDR strain, Genbank Accession Number M32078"
/replace="c"
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                                                                                         Toxicology, University
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Pred. No. 0.00e+00;
0; Mismatches 1402; Indels 136;
                     2 (bases 1 to 5068)
Miyazaki,M., Ohyama,K., Dunlap,D.Y. and Matsumura,F.
Direct Submission
Submitted (17-5EP-1996) Environmental Toxicology, Un
California at Davis/ITEH, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                              /product="para-type sodium channel"
/db_xref="PID:91633648"
                                                                                                                                   Location/Qualifiers
1. 5068
/organism="Blattella germanica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLEPPLQIHKPNKYKIVSMDM"
                                                                                                                                                                                                     /strain="CSMA"
/db_xref="taxon:6973"
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Local Similarity 70.4%;
hes 3659; Conservative
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Blattellinae;
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Cloning and sequencing of the para-type sodium channel gene from
susceptible and Kdr-resistant German cockroaches (Blattella
germanica) and house fly (Musca domestica)
Mol. Gen. Genet. 252 (1-2), 61-68 (1996)
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para-type sodium channel mRNA, partial cds
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    TGTGGGACTGCATGTACGTGGGGGATGTCTCGTGCATTCCCTTCTTGGCCACCGTTG
                                                                    TCATCGGCAATCTTGTGGTTCTTAACCTTTTCTTAGCCTTGCTTTTGTCAAATTTTGGCT
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oidea; Dictyoptera; Blattellidae;
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                                                                                                                                                                                                                                                                                                                                                  Score 696; DB 14; Length 98
Pred. No. 0.00e+00;
0; Mismatches 145; Indels
                                                               /note="similar to Drosophila para;
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  /gene="HF-para-b"
                                             /gene="HF-para-b"
                                                                                          /codon_start=1
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Similarity 85.3%;
841; Conservative
                  .>986
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/note="propagated on citrated bovine blood; DNA designated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-1998
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1 (bases 1 to 986)
Guerrero, F.D., Jamroz, R.C., Kammlah, D. and Kunz, S.E.
Guerrero, F.D., Jamroz, R.C., Kammlah, D. and Kunz, S.E.
pyrethroid-resistant horn files, Haematobia irritans:
identification of kdr and super kdr point mutations
Insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTGCAACAAACCAAATAGCGAGATTGGCTACCCGGGAGACTGTGGATCAGCTACTGTCG
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Guerrero,F.D., Jamroz,R.C. and Kunz,S.E. Briect Submission
Submitted (06-JAN-1997) USDA-ARS, Kniplii
Insects Research Laboratory, 2700 Freder
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Direct Submission
Submitted (06-JAN-1997) USDA-ARS, Knipling-Bushland Livestock
Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville,
TX 78028, USA
                                                                                                                                                                                        INV 07-APR-1998 alternatively spliced, partial cds.
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 1 GAGGGCTGGAATATTTTCGATTTCATTATCGTTGCCTTGTCTTTACTGGAATTGGGCCTG 60
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Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Muscoidea; Muscidae; Haematobia.
[ (bases 1 to 986)
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/organism="Haematobia irritans"
/organism="untreated pyrethroid-resistant"
/note="propasted on a steer without pyrethroid applications; DNA designated 'Super Res**"
/db_xref="taxon:7368"
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llarity 85.2%;
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Haematobia irritans
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AUTHORS
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                                                                                                   CACCAAGACAATAGACTGGAACATGAGCTAAACCATAGAGGTTTGTCCATACAGGACGAT
                                                   3321 GAGAGGACCAACCAGATCAGTTGGATTGGAGCGAAGAGCATGGTGACAACGAACAGGAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2901 CAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCTTTCCGGATGGCGACCTGCCG
                                                                                                                                                                                                                                                                                                                                        481 TTGTCCAATTTCGGTTCATCTAGTTTATCAGCACCGACTGCCGACAATGATACCAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781 CAACTGGAGGTGGCCATTGGCGATGGCATGGAGTTCACCATACATGGGGGATATGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         841 AACAAGCCCAAGAAATCAAAAATTCTTAAATAACACAACGATGATTGGAAACTCAATAAAC
GAGGGTCCCAGGGTCTGTCCGTATTGCGTTCCTTTCGATTGCTGCGTGTATTCAAACTG
                                 GCAAAATCTTGGCCCACCCTGAACTTACTCATTTCAATTACGGGCCGGACAATGGGTGCA
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Thackeray,J.R. and Ganetzky,B.
Conserved alternative splicing patterns and splicing signals in the
Drosophila sodium channel gene para
Genetics 141 (1), 203-214 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"sodium channel protein"
Alexaref-"piD:g1110414"
//translation-"FTED:g1104144"
AIGDGMEFTHGDMKNNFPKRSKYLNNATDDDTASINSYGSHKNRPFKDESHKGSAET
MEGEEKRADASKEDLGADGEDEGECECEPLGDIIHAHDEDILDEFRADESTY
KREPILAGDDDSPWGRLDLKFFFLIENKYFETAVITMILMSSLAL"
374 c 335 g 488 t
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            Eukaryotae: mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophildae; Drosophila.

1 (Dases 1 to 1840)
Thackeray J.R. and Ganetzky, B.
Developmentally regulated alternative splicing generates a complearry of Drosophila array of Drosophila as sodium channel isoforms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGACCATTCAAGGACGAGGCCACAAGGGCAGGCCGAGACGATGGAGGGCGAGGAGAA 1370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3659 TCGACCATTCAAGGACGAGGACCACAAGGGCAGCGCCGAGACGATGGAGGGCCGAGGAGAA 3718
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Thackeray,J.R. and Ganetzky,B.
Direct Submission
Submitted (10-MAY-1995) Justin R. Thackeray, Biology, Yale
University, 266 Whitney Avenue, New Haven, CT 06520, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAGGAGGCCCCGCTCGACGGTGATATCATTATTCATGCACGACGAGGATATACTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAATATCCAGCTGATTGCTGCCCCGATTCGTACTATAAGAAATTTCCGATCTTAGCCGG
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Pred. No. 0.00e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/map="X; 14C7-8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"FlyBase:FBgn0003036"
join(<405. .623,1267. .>1674)
/gene="para"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name="paralytic"
                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        405. .1674
/note="paralytic"
/gene="para"
                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="X"
405. .1674
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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Best Local Similarity 100.0%;
Matches 485; Conservative
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/strain="pyrethroid-susceptible"
/note="propagated on citrated bovine blood; DNA designated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-JAN-1997) USDA-ARS, Knipling-Bushland Livestock
Insects Research Laboratory, 2700 Fredericksburg Road, Kerrville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2661 GAGGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTATTGGAACTGGGACTC 2720
TGACGATGACTCGCCGTTCTGGCAAGGATGGGGCCAATTTACGACTGAAAACTTTTCAATT 1610
                                                                                                         3959 AATTGAAAATAAATATTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGC 4018
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                                          TGACGATGACTCGCCGTTCTGGCAAGGATGGGGCAATTTACGACACTGAAACTTTTCAATT 3958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to Drosophila para; splice variant A"
                                                                                                                                                                                                                                                        94/ bp mRNA INV 07-APR-199
Haematobia irritans para-like sodium channel (HF-para) mRNA,
U83871
92231544
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                                                                                  AATTGAAAATATATTTTGAAACAGCTGTTATCACTATGATTTAATGAGTAGCTTAGC
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1 (bases 1 to 94).

Guerrero, F.D., Jamroz, R.C., Kammlah, D. and Kunz, S.E. Toxicological and molecular characterization of pyrethroid-resistant horn flies, Haematobia irritans: Identification of Kdr and super-kdr point mutations insect Biochem. Mol. Biol. 27 (8-9), 745-755 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 947;
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Pred. No. 0.00e+00;
0; Mismatches 105; Indels
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/organism="Haematobia irritans"
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Guerrero,F.D., Jamroz,R.C. and Kunz,S.E.
Direct Submission
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/gene="HF-para"
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llarity 84.0%;
Conservative
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                                                                                            CGATGGAATTTCACCGATTTCATGCACTCCTTTATGATTGTGTTCCGAGTGTTATGTGGT
                                                                                                                          GAATGGATTGAATCCATGTGGGACTGCATGTATGTGGGGCGATGTCTCCTGTATACCATTC
                               TIGGGTAATCTAACATTIGTACTTIGCATTAICATCTTCATCTTIGCCGTTAIGGGAATG
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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Sun Sep 13 07:20:22 1998; MasPar time 249.45 Seconds 1217.927 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-554-424-7 (1-6513) from US08554424.seq 6513

1 TCTAGACGTTGGCCGCATAG......ACGCGAGTATTAGCTCTAGA 6513
AGATCTGCAACCGGCGTATC.....TGCGCTCATAATCGAGATCT Description: Perfect Score: N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD: 88822 seqs, 23323279 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1 Database:

Mean 10.185; Variance 5.490; scale 1.855 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Score Match Length DB ID
6513 100.0 6513 2
6513 100.0 6513 1
100.0
100.0
6513 100.0 6513 2
110 1.7 7218 1
60 0.9 7218 1
41 0.6 215 1
36 0.6 215 1
36 0.6 1809 2
39 0.6 5904 1
37 0.6 5962 3
37 0.6 5975 1
37 0.6 5975 1
30 0.5 33 1
30 0.5 33 2
30 0.5 33 1
30 0.5 33 2
30 0.5 33 1
31 0.5 75 1

MOLECULE TYPE: CDNA

6.37e-04		4.81e-05	4.81e-05	1.77e-04	4.81e-05	4.81e-05	6.37e-04	1.77e-04	2.25e-03	2.25e-03	.25		.25	2.25e-03	2.25e-03	2.25e-03	2.25e-03	2.25e-03	2.25e-03	2.25e-03	2.25e-03	2.25e-03	2.25e-03
Patent No. 5482709. Patent No. 5273901.	ce 6		Н	ö	Sequence 14, Applicati	Sequence 9, Applicatio	29	Ä	ý	ģ	ý	ģ	ģ	~	'n	13,	'n	Ļ	ď		Sequence 1, Applicatio	'n	'n
5482709-9 Pat 5273901-10 Pat			,	5215881-2 Pat	PCT-US96-0 Sec	PCT-US96-0 Sec	PCT-US93-0 Sec					PCT-US95-1 Sec	PCT-US95-1 Sec	us-08-068- sec	,			US-08-014- Sec	0	5206152-1 Pat	US-07-745- Sec	-08-246-	-08-453-
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ALIGNMENTS

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Sequence 7, Application PC/TUS9514378
SEPLICANT: Wall, Linda
APPLICANT: Hall, Linda
APPLICANT: Feng, Gouping
C TITLE OF INVENTION: PARA SODIUM CHANNEL
C TITLE OF INVENTION: PARA SODIUM CHANNEL
C TITLE OF INVENTION: PARA SODIUM CHANNEL
C TITLE OF SEQUENCES: 7
C CORRESPONDENCE ADDRESS: 7
C CORRESPONDENCE NOY D. Meredith
C STREET: P.O. Box 2000, 126 E. Lincoln Avenue
C CITX: Rahway
C STATE: New Jersey
C COUNTRY: GSA
C STATE: New Jersey
C COMPUTER READABLE FORM:
C COMPUTER READABLE FORM:
C COMPUTER: IBM PC Compatible
C OPERATING SYSTEM: PC-DOS/MS-DOS
C CURRENT APPLICATION DATA:
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PCT-US95-14378-7 STANDARD; DNA; UNC; 6513 BP.
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ATOREY/AGENT INFORMATION:
NAME: METERIAL, ROD,
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 1933;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nuller acid
STRANDEDNESS: single
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                                  CACAACCGGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTCGATTGCAGGGCAGCT
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OTHER
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1. No. 0.00e+00;
Mismatches 0;
1582
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qq	TGTCG	ACGICAGCCGGTIGGGAIGGIGIACIGGACGCCAITAICAAIGAGGAAGCAIGCG 5	22
δy	GICG	CGTCAGCCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGCG	52
q	521 ATCCA	CCCGACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCGTTGGAATAA	in i
οχ	CCA	cccacagegacaaaggctatccgggcaattgtggttcagcgaccgttggaataa	28
QQ	5581 CGTTT	CICCICICATACCIAGITATAAGCITITIGATAGITATTAATAIATGACATIGCIG ;	ف
δλ	81 CGTT	CTCTCTCATACCTATATAAGCTTTTTGATAGTTATTAATATGTACATTGCT	64
QQ	41 TCAT	CTGGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACG	70
οy	5641 TCATT	cicadaaciaiagicadeccaccaagagacgigcaagagggiciaaccgacgacg	0
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ΟŸ	CIA	GACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATAC	76
qq	5761 GCTAT	GATCAGCTGTCCGAATTCCTGGACGTTGGAGCCCCCGCTGCAGATCCACAAAC	5820
δy	CIA	GATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCCGCTGCAGATCCACAAAC	5820
QQ	5821 CGAAC	AAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACT	æ
Qy	GAA	AAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGGTGACCTCATGTACT	5880
g	5881 GCGTC	GACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGCAATCCGATAG	
Qγ	Ğ	GACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAG	4
qq	5941 AGGAG	TTGGTGAGATAGCGGCCCGGCTACGGAGGCTACGAGCCCCG	0
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Qy	GGA	gecegricaricegarecegesececegesecegareaaceaacegacegare	80
QQ	6181 CGCC	GGTGGAGATGGTAGTGTTAACGGTACTGCAGAAGGAGCTGCCGATGCCGATG	24
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qq	6241 AGAG	GTAAATAGTCCGGGTGAGGATGCAGCGGCGGCGGCAG	30
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QC	6301 CGGC	GGCGGCGGCACGACGGCGGGAAGTCCCGGAGCGGGTAGCG	_
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QQ	6361 CCGC	CGTTCTCGTGGAGAG	6420
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QQ	6421 ACTC	GCGATCGCCGAGCAT	648(
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SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                       COUNTER: USA
ZIP: 07065-0900
COMPUTER REABABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,339
                                                                                                                                              3: John W. Wallen III
P.O. Box 2000, 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                 Score 6513; DB 1;
Pred. No. 0.00e+00;
0; Mismatches 0
             6513
                                         ВР
                                                                                                                                                                                                                                                  ATORNEY AGENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 1933
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
      6481 CCCTCCAAGATGCACGCGAGTATTAGCTCTAGA
                                         DNA; UNC;
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Best Local Similarity 100.0%;
Matches 6513; Conservative
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US-08-337-339-7 STANDARD;
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                                                                                                ATATGGGCGTGCTCACCGAGAAGTGCATCAAGAAGTTCCCGCTGGACGGTCCTGGGGCA
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                                          TCCCGCCGGAATTGGCCTCCACTCCTCTGAGGATATCGATCCCTACTACAGCAATGTAC
                                                                                                                                                           TGTGGATGCTCGATTCAATCCGATACGTCGTGTGGCCATTTACATTCTAGTGCATC
                                                                                                                                                                                                                    CATTATTTTCCCTATTCATCACCACACATTCTCGTCAACTGCATCCTGATGATAGC
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1 ACGAATTGCAAAGGAAGGCCGAAGAAGAAGAGGCTGCCGAAGAGGGGGGGG	1 CGGAAGAAGCTGCCGCCGAAAGGGGCCAAGCTGGAGGGGGGGCCAATGGGCAGGCTC	1 AGGCAGCAGCGGATGCGGCTGCCGAAGAGGCTGCACTGCATCCGGAAATGGCCAAGA	GTCCGACGTATTCTTGCATCAGGTATGAGCTATTGTTGGCGGCGAGAGGCAACGATG	1 ACAACAACAAAGAGAAGATGTCCATTCGGAGCGTCGAGGTGGAGTCGGAGTCGGTGAGCG	1 TTATACAAAGACAACCAGCACCTACCACAGCACACCAAGCTACCAAAGTTCGTAAAGTGT 	1 GCACGACATCCTTATCCTTACCTGGTTCACCGTTTAACATACGCAGGGGATCACGTAGTT	1 CTCACAAGTACACGATACGGAACGGACGTGCCGCTTTGGTATACCCGGTAGCGATCGTA	AGCCATTGGTATTGTCAACATATCAGGATGCCCAGCAGCACTTGCCCTATGCCGACGACT	1 CGAATGCCGTCACCCGGATGTCCGAAGAGAATGGGGCCATCATAGTGCCCGTGTACTATG	GCAATCTAGGCTCCCGACACTCATCGTATACCTCGCATCAGTCCCGAATATCGTATACCT	CACATGGCGATCTACTCGGCGGCATGGCCGTCATGGCGCGTCAGCACAATGACCAAGGAGAA 	1 GCAAATTGCGCAACCGCAACACGCAATCAATCAGTGGGGGCCACCAATGGCGGCACCA	CCTGTCTGGACACCAATCACAAGCTCGATCATCGCGACTACGAATTGGCCTGGAGTGCA	61 CGGACGAAGCTGGCAAGATTAAACATCATGACAATCCTTTTATCGAGCCCGTCCAGACAC	11 AAACGGTGGTTGATATGAAAGATGTGATGGTCCTGAATGACATCATCGAACAGGCCGCTG 	11 GTCGGCACAGTCGGCAAGCGATCGCGGTGTCTCCGTTTACTATTTCCCAACAGAGGACG	1 ATGACGAGGATGGGCCGACGTTCAAAGACAAGGCACTCGAAGTGATCCTCAAAGGCATCG 	1 AIGIGITITIGIGIGAGACIGITGCIGGGITITGGITGAAAITICAGGAGIGGGIAAICGC
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q	2461	TCATCGTCTTCGATCCCTTCGTCGAGCTCTTCATCACGCTGCATTGTGGTCAACACGA 2520
da	52	GTTCATGGCAATGGATCACCACGATATGAACAAGGAGATGGAACGCGTGCTCAAGAGTG 258
δy	2521	TGTTCATGGCAATGGATCACCACGATATGAACAAGGAGATGGAACGCGTGCTCAAGAGTG 2580
qq	2581	GCAACTATTTCTTCACCGCCACCTTGCCATCGAGGCCACCATGAAGGCCATGA 2640
δλ	2581	CAACTATTICITCACCGCCACCITIGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 264
q	2641	CCCAAGTACTATTTCCAGGAGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT 270
δλ	2641	CCCCAAGTACTATTTCCAGGAGGCTGGAACATCTTCGACTTCATTATCGTGGCCCTAT
q	2701	CTATTGGAACTGGGGACTCGAGGGTGTCCAGGGTCTGTCCGTATTGCGTTCCTTTCGAT 276
٥y	2701	GCTATTGGAACTGGGACTCGAGGTGTCCAGGGTCTGTCCGTATTGCGTTCCTTTCGAT 276
q	2761	GCGTGTATTCAAACTGGCCAAGTCTTGGCCCACATAATTTACTCATTTCGATTA 282
Qy	2761	GCTGCGTGTATTCAAACTGGCCCAAGTCTTGGCCCACACTTAATTTACTCATTTCGATTA 28
qq	2821	ACGCACCATGGGCCTTTGGGTAATCTGACATTGTACTTTGCATTAT
Οy	2821	GGGACGCACCATGGGCGCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTCA 28
QQ	2881	ITTGCGGTGATGGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCT 294
Qy	2881	CTTGCGGTGATGGGAATGCAACTGTTCGGAAAGAATTATCATGATCACAAGGACCGCT 294
qq	2941	CCGGATGGCGACCTGCCGCGCTGGAACTTCACCGACTTTATGCACAGCTTCATGATCG 300
Qy	2941	TCCGGATGGCGACCTGCCGCGCTGGAACTTCACCGACTTTATGCACAGCTTCATGATCG 300
QQ	3001	TICCGGGTGCTCTGCGGAGAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGCG 306
Qy	3001	GTTCCGGGTGCTCTGCGGAGAATGGATCGAGTCCATGTGGGACTGCATGTACGTGGGC
qq	3061	SICTCGIGCATICCCTICTICGCCACCGTIGTCATCGGCAATCTIGTGGTACTTA 312
Qγ	3061	ICTCGTGCATTCCCTTCTTCTCGCCACCGTTGTCATCGGCAATCTTGTGGTACTTA 312
QQ	3121	CITITCITAGCCTIGCTITIGTCCAAITTIGGCTCAICTAGCGCTAICAGCGCCGACTG 318
Qy	3121	CITITICITAGECTITICITECTATITICGCTCATCTAGCTTATCAGCGCCGACTG 31
q	3181	TAAAATAGCCGAGGCCTTCAATCGAATTGGCCGATTTAAAAGTT 3
Qy	3181	CGATAACGITACGATAAGATAAGAGCCTTCAATCGAATGGCCGATTAAAAGTT 32
QQ	3241	TTAAGCGTAATATTGCTGATTGTTTCAAGTTAATACGTAACAAATTG
δλ	3241	GGTTAAGCGTAATATTGCTGATTGTTTCAAGTTAATACGTAACAAATTGACAAATCAAA 33
QQ	3301	STGATCAACCATCAGGTGAGACCAACCAGATCAGTTGGATTTGGAGGGAG
δλ	3301	AAGTGATCAACCATCAGGTGAGGACCAACCAGATCAGTTGGATTTGGAGGGAAGAGC 336
qq	3361	GGTGACAACGAACTGGAGCTGGGCCACGACGAGATCCTCGCCGACGGCCTCATCAAGA 3
δλ	3361	TGGTGACAACGAACTGGAGCTGGGCCACGACGAGATCCTCGCCGACGCCTCATCAAGA 342
qq	3421	3GGATCAAGGAGCAGACGCAACTGGAGGTGGCCATCGGGGATCGGATGGAATTCACGA 3
QY	3421	CGA 348
QQ	4	CACGGCGACATGAAGAACAAGCCGAAGAAATCCAAATATCTAAATAAGGCAACGA 354
οy	3481	CACGCCACATGAAGAACAAGCCGAAGAATCCAAATATCTAAATAACGCAACGA 35

	4681 TATATTTCGTATT 	4741 TTATCATTGATAA 	4801 TGACAGAAGATCA 	4861 TAAAAGCCATTCC 	4921 ATAAGAAATTCGA 	타그타	TCGTA TCGTA	5101 TTATTGAGCCATG 		5221 TGGCGAAAGTGGG 		5341 TCATGTTCATCTT	5401 GCATTAACGACGT 	5461 TGTCGACGTCAGC	5521 ATCCACCCGACAG	5581 CGTTTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC		S/OI ACTACGACATGIA
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3541 TGATTGGCAACTCAATTAACCACCAAGACAATAGACTGGAACACGAGCTAAACCATAGAG 3600 	3601 GTTTGTCCTTACAGGACGACGACGCAGCATTAACTCATATGGTAGCCATAAGAATC 3660 	r) r)	3721 GCGACGCCAGCAAGGAGATTTAGGTCTCGACGAGGAGACGGGAGAGAGGGGGATGGG 3780 	3781 AGGAGGCCCGCTCGACGGTGATATCATTATTCATGCACACGACGAGGATATACTCGATG 3840 	3841 AATAICCAGCIGATIGCIGCCCGAITCGTACTATAAGAAATTICCGAICTIAGCCGGIG 3900 	3901 ACGATGACTCGCCGTTCTGGCAAGGATGGGCAATTTACGACTGAAAACTTTTCAATTAA 3960 	3961 TTGAAAATAATATTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCTT 4020 	4021 TGGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTTATACTATA 4080 	4081 TGGACAGAATATTACGGTTATATTCTTCTGGAAATGTTAATCAAGTGGTTGGCGCTCG 4140 	4141 GCTTCAAAGTGTACTTCACCAACGCGTGGTGTTGGCTCGATTTCGTGATTGTCATGGTAT 4200 	4201 CGCTTATCAACTTCGTTGCTTCACTTGTTGGAGCTGGTGGTATTCAAGCCTTCAAGACTA 4260 	4261 TGCGAACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCCGTATGCGGGCATGAGGG 4320 	4 4	4381 TAATATITTGGCTAATTTTGCCATAATGGGTGTACAGCTTTTTGGTGGAAATATTTTA 4440 	4441 AGTGCGAGGACATGAATGGCACGAAGCTCAGCCACGAGATCATACCAAATGCCAATGCCT 4500 	501 GCGAGAGCGAGAACTACACGTGGGTGAATTCAGCAATGAATTTCGATCATGTAGGTAACG 4560 	CGTATCTGTGCCTTTTCCAAGTGGCCACCTTCAAAGGCTGGATACAAATCATGAACGATG	621 CTAICGAITCACGAGAGGIGGACAAGCAACCAAITCGIGAAACGAACAICIACAIGIAII 4680
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GGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTG SCCATGTGCCTCCCGGCCCTGTTCAACATCTGCCTGCTGCTGTTCCTGG ACTATGAGATCTGGCAGCAATTCGATCCGGAGGCACCCAGTACATAC TCTTCATCATATTTGGATCCTTTTCACACTCAATCTGTTCATTGGTG TTATCGAGAAGTACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGCGTG GCCGTGTCCTTCGACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGC TTGCCATTTTCGGCATGTCGTTCTTCATGCACGTGAAGGAGAAGAGCG CCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGCG GCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCGTTGGAATAA CATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGCTG ACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACG TCAGTTCCGAATGTCTATTAAAATATTCGCTTTACGATATCACTATT **ATATAATCATTATGTTATTCATTGGTCTGAACATGTTCACCATGACCC**

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1 TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC
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SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER
                                                                                                                                                                                                                                                                                                           Score 6513; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                   SOFTWARE: FASTSeq. Version #1.d5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,095
                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         CLASSIFICATION: 536
ATORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1933
TELEPHONE: (908) 594-3905
TELEPHONE: (908) 594-305
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHRARATICS:
LENGTH: 6513 base pairs
TYPE: NUCLEic acid
STRANDENESS: single
                                                     disk
                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6513; Conservative
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 Rahway
New Jersey
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                     Y: USA
07065-0907
                                                                                                                     FILING DATE:
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CITY: Rab
STATE: Ne
COUNTRY:
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                                GCGTCGACATCCTCGACGCCCTTACGAAAGACTTCTTTGCGCGGAAGGGCAATCCGATAG
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                     GCTATGATCAGCTGTCCGAATTCCTGGACGTACTGGAGCCCCCGCTGCAGATCCACAAAC
                                                               CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACT
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APPLICANT: Hall, Linda
APPLICANT: Hall, Linda
APPLICANT: Ferg, Gouping
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXP
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. Mark Hand - Merck & Co., Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JT 3
US-08-724-095-7 STANDARD; DNA; UNC; 6513
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Sequence 7, Application US/08724095
Patent No. 5688917
GENERAL INFORMATION:
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1681	1741	1741	1801	1861	1861	1921	1921	1981	1981	2041	2041	2101	2101	2161	2161	2221	2221	2281	2281	2341	2341	2401	2401	2461	2461	2521	5	2581	2581	2641	2641	2701	2701	2761
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qq	3961	TIGAAAATAAATTITIGAAACAGCIGTTATCACTATGATTTTAATGAGTAGCTTAGCT
Qy	3961	TGAAAATAAATATTTTGAAACAGCTGTTATCACTATGATTTTAATGAGTAGCTTAGCT
qa	2	80
δλ	4021	GGCATTAGAAGATGTACATCTGCCACAAAGACCCATACTGCAGGATATTTTATACTATA 408
Q	4081	TGGACAGAATATTTACGGTTATATTCTTCGAAATGTTAATCAAGTGGTTGGCGCTCG 4140
δλ	4081	GACAGAATATTTACGGTTATATTCTTCGAAATGTTAATCAAGTGGTTGGCGCTCG 414
QQ	4141	GCITCAAAGIGIACITCACCAACGCGIGGIGIIGGCICGAITICGIGAITGICAIGAT 4200
δy	4141	CTTCAAAGTGTACTTCACCAACGCGTGGTGTTGGCTCGATTTCGTGATTGTCTTTT 420
qq	4201	CITCGITGCTTCACTIGITGGAGCTGGTGTATTCAAGCCTTCAAGACTA 4
Qy	4201	GCTIATCAACTICGTIGCTICACTIGTIGGAGCIGGIGGIATICAAGCCTICAAGACTA 426
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٥y	4261	GCGAACGTIAAGACCACTGAGACCACTACGTGCCCATGTCCCGTATGCAGGCATGAGGG 432
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٥y	4321	CGTCGTTAATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGT 438
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Oy	4621	ATCGATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACG
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qq	4741	ATCATTGATAATTTTAATGAGCAAAAAAAAGCAGGTGGATCATTAGAAATGTTCA 48
QY	4741	TATCATTGATAATTTTAATGAGCAAAAAAAAAAAGGTGGTGGTCATTAGAATGTTCA 480
qq	4801	TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAGATGGGCTCTAAAAAACCAT 4860
ΟŊ	4801	GACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAAACAT 48
q	4861	TABARGCCATTCCARGACCAAGGTGGCGACCACAAGCAATAGTCTTTGAAATAGTAACCG 4920
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qq	4921	ATAAGAAATTCGATATAATCATTATTTTATTGTCTGAACATGTTCACCATGACC 4980
٥y	4921	ATAAGAAATTCGATATAATCATTATTCATTGGTCTGAACATGTTCATGACC

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CGCCCGCTGGTGGAGATGGTAGTGTTAACGGTACTGCAGAAGGAGGTGCCGATGCCGATG
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Sequence 7, Application US/08338702
Patent No. 5550049
GENERAL NO. 5550049
GENERAL NO. MARMAL OFFICE W.
APPLICANT: Warmke, Jeffrey W.
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXP
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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STREET: P.O. Box 2000, 126 E.
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 1933(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
                                                                                                                                                                                                                                                                                                                   US-08-338-702-7 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS:
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Quer Best Matc	Y M Lo	atch 100.0%; Score 6513; DB 1; Length 6513; cal Similarity 100.0%; Pred. No. 0.00e+00; 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	т т	TCTAGACGTTGGCCGCATAGACAATGACAGAAGATTCCGACTCGATATCTGAGGAAGAAC 60 	
	61	GCAGTITGITCCGTCCCTTTACCCGCGAATCATTGGTGCAAATCGAACAACGCATTGCCG 120 	
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	421	TGTGGATGCTCGATCCATTCAATCCGATAGGTCGTGGCCATTTACATTCTAGTGCATC 480 	
	481	CATTAITITCCCTAITCATCATCACCACAATICTCGTCAACTGCATCCTGATGATAATGC 540 	
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	721	TAGGTAATCTAGCAGCCCTGCGAACGTTTAGGGTGCTGCGAGCGCTTAAAACCGTAGCCA 780 	
	781	TIGIGCCAGGCIIGAAGACCAICGICGGCGCCGTCAICGAAICGGTGAAGAATCTGCGCG 840	
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à	, 0	CCTGTCTGGACACCAATCACAAGCTCGATCATCGCGACTACGAAATTGGCCTGGAGTGCA 216	Qy	31
1 6	2161	CCC	qq	32
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: A	2581	GCAACTATTCTTCACCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 264	qq	36
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à	2821	TGGGACGCACCATGGGCGCTTTGGGTAATCTGACATTGTACTTTGCATTATCATCTTCA 288	٥y	39
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8 8	3061	AIGICICGAGATICCCTICTITICALITY AIGICAATCGGAATCTTGTGGTAATTAA 312	QY	41
· අ	3121	ACCITITCITAGCCITGCITITGCCCAATTTGGCTCATCTAGCTTATCAGCGCGCCGACTG 318	qq	42
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		SACATGAATGCCACGAAGCTCAGG SAGAACTACACGGGGGGGGAATTC2 SAGAACTACACGGGGGGGGGAATTC3	TGCCTTTTCCAAGTGGCCACCTTCA 	TCACGAGAGGTGGACAAGCAACCAA 	CGTATTCTTCATCATATTTGGATCCT" 	IGATAATTTTAATGAGCAAAAGAAAAAGC 	aagatcagaaaagtactataatgctat 	CATTCCAAGACCAAGGTGGCGACCAC 	CGATATAATCATTATGTTATT 	TTACGATGCGTCGGACACGTATAACGC 	TATTTCAGTTCCGAATGTC: 	GCCATGGAATTTATTTGATGTAGTA 	CGATATTATCGAGAAGTACTTCGTGT 	STGGGCCGTGTCCTTCGACTGGT 	GTTGGCCATGTCGCTGCCGGCCCI	CATCTTTGCCATTTTCGGCATGTC
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APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
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SEQUENCE 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 OTHER.
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                                                                                                                                                                                                                                                                              ZIE: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                      Lincoln Avenue
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Pred. No. 0.00e+00;
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PCT-US95-14262-7 STANDARD; DNA; UNC; 6513
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PC/TUS9514262
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NAME: Tribble, Jack L.
REGISTRATION UNDRER: 32,633
REFERENCE/DOCKET UNDRER: 1933E
TELECOMMUNICATION INFORMATION:
TELEFAX: (908) 594-5321
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                          3: Jack L. Tribble
P.O. Box 2000, 126
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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Local Similarity 100.0%;
nes 6513; Conservative
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                                                                                                                                                                                                                                    STREET: P.O. BOX 20
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
                                                                                                                       Sequence 7, Application Sequence 7, Application
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                                                                                                                                             GENERAL INFORMATION:
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SCTGCCGCCCAAAGCGGCCAAGCTGGAGGAGCGGGCCAATGCGCAGGCTC SCTGCCGCCGCCAAAGCGGCCAAGCTGGAGGAGCGGGCCAATGCGCAGGCTC SCGGATGCGCCCCCCCAAAGCTGGAGGAGGCGGGCCAATGCGCAAGGCTC SCGGATGCGGCCGCCGAAGAGCTGCATCCGGAAATGGCCAAGA GCGGATGCGGCTGCCGCAAGAGGCTGCATCCGGAAATGGCCAAGA HITTCTTGCATCAGCTATTGTTGTTGCCGCGCGAAATGGCCAAGA TATTCTTGCATCAGCTATTGTTGTGGCGCGCGAAAGGGCAACGGTG TATTCTTGCATCAGCTATTGTTGTTGCGGCGAGAAGGGCAACGGTG TATTCTTGCATCAGCTATTGTTGTTGCGGCGAGAAGGGCAACGGTG TATTCTTGCATCAGCTATTTGTTGCGGCGCGAGAAGGGCAACGGTG TATTCTTGCATCAGCTATTTGTTGCGGCGCGGAGAGGGCAACGGTG TATTCTTGCATCAGCTATTTGTTGCCGAGTTGCGAGTGCGTGAGCGCAACGGTCCGTGAGCGCCAACGGTCGCAAGTCGCAACTCCAACTCCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCGCAACTCAACTCAACTAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACT	MAGAGAGATECCATTCGGAGCGTCGAGSTGGAGTCGAGTCGGAGTCGAGAGCGAGGGAGTCGAGAGTCGAGTCGGAGGTGGAGTCGAGAGTCGAGTCGAGTCGAGTCGGAGTCGGAGTCGGAGTCGGAGTCGGAGTCGGAGTCGGTGAGCGGGAGTCGGAGGTCGGAGGTCGGTGAGCGGGGTGGAGTCGTAAAGTGAGTTTTTTTT	CCTTATCCTTACCTGGTTCACCGTTTAACATAGGCAGGGATCACGTAGTT ACACGATACGGAACGGA	3TCACCCCGATGTCCGAAGAGAATGGGCCCATCATAGTGCCCGTGTACTATG STCACCCCGATGTCCGAAGAGAATGGGCCCATCATAGTGCCCGTGTACTATG STCACCCCGATGTCCGAAGAGAATGCCCCCATCATAGTGCCCGTGTACTATG SGCTCCCCGAATGTCGTATACCTCGCATCAGTCCCGAATATCGTATACCT IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	SCATCTACTCGCCGCGATGGCCGTCAGGCGGTCAGCAATGACCAAGGAA [1111111111111111111111111111111	AAGCTGGCAAGATTAAACATCATGACAATCCTTTATCGAGCCCGTCCAGACAC
5GAAGA 6GAAGA 6GCAGC 11111 6GCAGC TCCGAC	ACAACAACAA 	CACGAC TCACAA TCACAA TCACAA TCACAA	VATGC	CACATGG 	CGGACGA AAACGGT AAACGGT GTCGGCA GTCGGCA ATGACGA ATGACGA ATGACGA
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GTCAACACGA GTCAACACGA	CTCAAGAGTG 	rggccarg rggccarg	GIGGCCCIAT GIGGCCCIAI	CTTT	TTTCGATT 	TATCATCTTC TATCATCTTC	U U	TTCATGATC TTCATGATC	TACGTGGGCG	GTGGTACTT	GCGCCGACTC	GCGCCGACT	TTTAAAAGTT TTTAAAAGTT	ACAAATCAA	ACAAATCAA	AGCGAAGAG 	CICATCAAG	CTCATCAAC	GAATTCACG		AACGCAACG		
TGCATTGTGG TGCATTGTGG	AACGCGTG AACGCGTG	ATGAAGCT ATGAAGCT	FICATTAIC 	STATTGCGT	AATTTACT AATTTACT	CTTTGCAT	rgarcac rgarcac	TATGCACAGC TATGCACAGC	CTGCATG 	GGCAATCTT	AGCTTATCA	AGCTTATCA	ATTGGCCGA 	PACAAATTG	AACAAATTG	TGGATTTGG	GCCGACGC	GCCGACGGC	GATCGGATG	SGATCGGATC	TATCTAAAT	ATATCTAAAT	ACACGAGCT?
ATCACGCTG1 ATCACGCTG1	AGGAGAT AGGAGAT	AGGCCACC 111111 AGGCCACC	CCTCGAC 	1016100 	ACACTI 	ACATTTGTA 	AAGAATTAT AAGAATTAT	ACCGACTTT ACCGACTTT	TCCATGTGG TCCATGTGG	GTTGTCATC	GGCTCATCT	GGCTCATCT	TTCAATCGA	TTAATACGT	TTAATACGI	CAGATCAGI CAGATCAGI	GAGATCCTC	GAGATCCTC	GCCATCGG	seccarcee	SAAATCCAA	SAAATCCAAA	PAGACTGGA
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δ	4621	CTATCGATTCACGAGAGGTGGACAAGCAACCAATTCGTGAAACGAACATCTACATGTATT .	4680
q	4681	ATTICGIATICITCATCATATITGGATCCTTTTTCACACTCAATCTGTTCATTGGT	4
οy	4681	ATATITICGTATICTICATCATATITICGATCCTITITICACACTCAATCTGTTCATIGGT	4740
đ	4741	TATCATTGATAATTTTAATGAGCAAAAGAAAAAAGCAGGTGGATCATTAGAAATGTTC	
οy	4741	TTATCATTGATAATTTTAATGAGCAAAAGAAAAAGCGGGGGGGTCATTAGAAATGATCA	0
QQ	4801	TGACAGAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT	4860
οy	4801	Gacagaagatcagaaaagtactataaatgctatgaaaagatggggtgtaaaaaag	9
q	4861	TAAAAGCCATTCCAAGACCAAGGGGGGCGACCACAAGCAATAGTTTGAAATAGTAACCG	4920
QΫ	4861	CATICCAAGACCAAGGIGGCGACCACAAGCAAIAGICTITGAAATAGIAACC	2
ପୁପ	4921	ATAAGAAATTCGATAAATCATTATGTTATTCATTGGTCTGAACATGTTCACGATGACC	æ
δy	4921	aagaaaticgatataatcattatgttattcattggtctgaacatgttcaccatgacc	98
q	4981	TCGATCGTTACGATGCGTCGGACACGTATAACGCGGTCCTAGACTATCTCAATGCGATAT	5040
Qy	4981	CGATCGTTACGATGCGTCGGACACGTATAACGCGGTCCTAGACTATCTCAATGCGAT	04
තු	5041	TCGTAGTTATTTTCAGTTCCGAATGTCTATTAAAATATTCGCTTTACGATATCACTATT	5100
QY	5041	CGTAGTTATTTTCAGTTCCGAATGTCTATTAAAAATATTCGCTTTACGATATCACTAT	2100
đ	0	TTATTGAGCCATGGAATTTATTTGATGTAGTAGTTGTCATTTTATCCATCTTAGGTCTTG	16
οy	0	tattgagccatggaatttatttgatgtagtagttgtcattttatccatcttaggtctt	5160
අු	9	TACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCCGACCCTGCTCCGAGTGGTGCGTG	5220
Qy	5161	acttagcgatattatcgagaagtacttcgtgtcgccgaccctgctccgagtggtgc	7
qa	5221	TGGCGAAAGTGGGCCGTGTCCTTCGACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGC	5280
Qy	5221	GGCGAAAGTGGGCCGTGTCCTTCGACTGGTGAAGGGAGCCAAGGGCATTCGGACACTG	5280
අ	5281	TCTTCGCGTTGGCCCATGTCGCTGCTGCCTGTTCAACATCTGCTGCTGTGTTCCTGG	5340
Qy	5281	CTICGCGTTGGCCATGTCGCTGCTGCTTCAACATCTGCCTGCTGCTGTTCCTG	(C)
q	5341	CATITICGCCAIGICGIICII	5400
ΟŊ	5341	CATGITCATCITIGCCATTITCGGCATGITCTTCTTCATGCACGIGAAGGAAGAGG	5400
ф	5401	GCATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTTCAGA	5460
QY	5401	CATTAACGACGTCTACAACTTCAAGACCTTTGGCCAGAGCATGATCCTGCTCTTTCAG	4
qq	5461	GTACTGGACG	5520
Qy	5461	GTCGACGTCAGCCGGTTGGGATGGTGTACTGGACGCCATTATCAATGAGGAAGCATGC	S
qq	5521	CACCCGACAGCGACAAAGGCTATCCGGGCAATTGTGGTTCAGCGAC	5580
Qy	5521	JCACCCGACACAAAGGCTATCCGGGCAATTGTGGTTCAGCGACCGTTGG	ß
q	5581	TCCTCTCATACCTATATAAGCTTTTTGATAGTTATTAATATGTACCT	5640
Qy	5581	GTITCTCCCTCTCATACCTAGTTATAAGCTTTTTGATAGTTATTAATATGTACATTGC	5640
qa	5641	TCATICTCGAGAACTATAGICAGGCCACCGAGGACGTGCAAGAGGGTCTAACCGACGACG	5700
Qy	5641	ATTCTCGAGAACTATAGTCAGGCCACCGAGGACGTGCAAGAGGGTCTAACCGACGAC	2700
qa	5701	ACTACGACATGTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATAC	9160
Οy	5701	IACGACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACAT	2760

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                                                                                           CGAACAAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGTGACCTCATGTACT
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VS
COUNTRY: USA
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US-08-232-463-14 STANDARD; DNA; UNC; 7218
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.7%; Score 110; DB 1; Length 7218; Similarity 1.9%; Pred. No. 2.08e-58; 7; Conservative 237; Mismatches 134; Indels
                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                            29,768
FR: 30472/114 IMMU
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US-08-232-463-14 STANDARD; DNA; UNC; 7218
                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300
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                                                                                                                                                                                                                                                                                                FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECHONE: (703)836-9300
TELEX: 999149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity
Matches 7; Conser
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REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDENESS: single
          /T 8
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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Matches 30; Conservative
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ZIP: 94105-1493
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
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197; Mismatches 143; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22313-0299
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
     APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKINER, F. G.
TILE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/ORCKET NUMBER: 3472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703)683-4109
                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match

0.9%; Score 60;
Best Local Similarity 1.7%; Pred. No. Matches 6; Conservative 197; Misman
                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                         CITY: Alexandria
 SENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                       FILING DATE:
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Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
CC GENERAL INFORMATION:
CC GENERAL INFORMATION:
CC APPLICANT: LABAVITCH, John M.
APPLICANT: STOTZ, Henrik
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
CC CORRESPONDENCE ADDRESS:
CC CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC STATE: California
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: : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | | :: : : | | :: : : | | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : | | | :: : : | | | :: : : | | | :: : : | | :: : : | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | :: : : | | | :: : : | | :: : : | | :: : : | | :: : : | | :: : : : : : : | | :: : : | | :: : : | | :: : : : | | | :: : : | | :: : : | | :: : : : | | :: : : | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | | :: : : | | :: : : | | :: : : | | :: : : : | | :: : : | | | :: : | | | :: : : | | | :: : : | | | :: : : | | :: : : | | | :: : : |
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LOCATION: 1.215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1; Length 215;
Pred. No. 2.09e-10;
77; Mismatches 83; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
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Gaps
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Sequence 6, Application US/07745206A
Sequence 6, Application US/07745206A
C Patent No. 5429921
C BAPPLICANT: Harpold, Michael
APPLICANT: Harpold, Michael
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: sig_peptide
LOCATION: 255..324
SEQUENCE 1809 BP; 342 A; 590 C; 504 G; 373 T; 0 OTHER.
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                                                                                                                                                                                                               UVELCATURE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFRENCE/DOCKET NUMBER: HMI-OILCPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENDTH: 1809 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 11
US-07-745-206A-6 STANDARD; DNA; UNC; 5904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: both
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1..264
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LOCATION:
FEATURE:
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FEATURE:
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APPLICANT: BENNETT, Alan
APPLICANT: LABATTCH, John M.
APPLICANT: LABATTCH, John M.
APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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LOCATION: 1..215
OTHER INFORMATION: /Standard_name= "Deduced amino acid
OTHER INFORMATION: Sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 215;
Pred. No. 2.27e-07;
61; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                 STALL:
COUNTRY:
US
ZIP: 94105-1493
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBAM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKH 160
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PCT-US95-11869-1 STANDARD; DNA; UNC; 1809 BP.
XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY-AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
             .T 9
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                       Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%;
Best Local Similarity 16.9%;
Matches 27; Conservative
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5307 GCCCTGTTCAACAICTGCCTGCTGTTCCTGGTCATGTTCATCTTTTGGCC 5366
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Sequence 1, Application US/08404354B
Patent No. 5618720
GENERAL INFORMATION:
APPLICANT: Bills, Steven Bradley
APPLICANT: Harbold Michael Miller
APPLICANT: Barbold Michael Miller
APPLICANT: Schwartz, Arnold
APPLICANT: Schwartz, Arnold
APPLICANT: Renenc, Robert
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
                                                                                                       .T 13
US-08-404-354B-1 STANDARD; DNA; UNC; 5975 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence
LOCATION: 79...5700
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 5975 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%;
Best Local Similarity 65.0%;
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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                                        3982 ATG 3984
                                                                5367 ATG 5369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  3819 AAICGCCAIGAACAICCTCAACAIGCTCTICACIGGCCTCTICACCGTGGAGAIGAICCI 3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2564 ACGCGTGCTCAAGAGTGGCAACTATTCTTCACCGCCACCTTGCCATCGAGGCCACCAT 2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3879 GAAGCICATIGCCTICAAACCCAAGGGITACTITIAGIGAICCCIGGAAIGTITITIGACTT 3938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2624 GAAGCTAATGGCCATGAGCCCAAGTACTATTTCCAGGAGGGCTGGAACATCTTCGACTT 2683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3862 CTGCTGAGTCGGGCCGAGGCGTGCGCACGCTGCTGGACGTTCATCAAGTCCTTCCAG 3921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5247 CTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCTGCCG 5306
                                                                                                                                                                                                                                                                                                                                                                                                             3922 GCCCTGCCCTACGTGGCCCTGCTCATCGTCATGCTGTTCTTCATCTACGCCGTCATCGGC 3981
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Patent No. 5386025.
Patent No. 5386025
APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN B.; HARPOLD, MICHAEL
M.; CAMPBELL, KEVIN P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
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LENGTH: 5962
Sequence 6459 BP; 1280 A; 1835 C; 1691 G; 1156 T; 497 other;
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
SEQUENCE 5904 BP; 1353 A; 1717 C; 1544 G; 1260 T; 30 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5962;
                                                                                                                                                                                                                                                                                                                                            Score 39; DB 1; Length 5904; Pred. No. 3.54e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 3; Length 5962;
Pred. No. 5.73e-08;
0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 75; Indels
                                  COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19910815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/482,384
FILING DATE: 20-FEB-1990
                                                                                                                                        CLASSIFICATION: 435
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: FEGER, SCOLT B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7T 12
5386025-5 STANDARD; DNA; UNC; 6459 BP
                                                                                                                                                                                                                                               LENGTH: 5904 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%;
Best Local Similarity 60.3%;
Matches 114; Conservative
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Best Local Similarity 65.0%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                        unknown
Illinois
              U.S.A.
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             COUNTRY:
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Pred. No. 5.73e-08;
0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 5975 BP; 1291 A; 1832 C; 1695 G; 1157 T; 0 OTHER.
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEGO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,354B
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL.1992
APPLICATION NUMBER: US 07/603,751
FILING DATE: US 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
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3814 CTGCTGAGTCGGGCCGAGGGCGTGCACGCTGCTGTGGACGTTCATCAAGTCCTTCCAG 3873
         3874 GCCCTGCCCTACGTGGCCCTGCTCATCGTCTTCTTCATCTACGCCGTCATCGGC
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                5247 CTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCTGCCG 5306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Coding Sequence
LOCATION: 79...5700
OTHER INFORMATION:
SEQUENCE 5975 BP; 1291 A; 1832 C; 1695 G; 1157 T; 0 OTHER.
                                                                                                                                                                                                            ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
                                                                                    T 14
US-08-314-083B-1 STANDARD; DNA; UNC; 5975 BP.
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,083B
FILING DATE: 28-SEPT-1994
CLASSIFICATION: 435
PRIOR APPLICATION ATS
APPLICATION WHERE: US/08/314,083B
FILING DATE: 13-JUL-1992
RIGH APPLICATION NUMBER: US/08/3151
FILING DATE: 08-NOV-1990
ATTORNEY/AGENT INFORMATION:
AMME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
RECISTRATION NUMBER: 33,779
RECISTRATION NUMBER: 33,779
RECISTRATION NUMBER: 33,779
RECISTRATION NUMBER: 33,779
RETERECOMMUNICATION NUMBER: 33,779
TELEPHONE: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6%;
Best Local Similarity 65.0%;
Matches 80; Conservative
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                                                                                                                                                                                                                                                   92101-2926
                                                                                                                                                                                                                                              USA
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                                               3934 ATG 3936
                                                              5367 ATG 5369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFOGRATION:
APPLICANT: Warmke, Jeffrey W.
APPLICANT: Hall, Linda
APPLICANT: Feng, Goupinda
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE
TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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STREET: P.O. Box 2000, 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 1; LA
Pred. No. 6.37e-04;
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SEQUENCE 33 BP; 10 A; 8 C; 9 G; 6 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                7 15
US-08-337-339-1 STANDARD; DNA; UNC; 33 BP.
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                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08337339 Sequence 1, Application US/08337339 Patent No. 5593864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W
REGISTRATION NUMBER: 35,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 33 base pairs
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Best Local Similarity 100.0%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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5367 ATG 5369
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	ALIGNMENTS RESULT ID T18986 standard; CDNA; 6513 BP. ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS B Drosophila para voltage-activated sodium channel; cation channel; tipE; KW antisense; ss. OS Drosophila melanogaster. BN WOSGISZO-A1. PR G-NOV-1995; UL4378. PR (MERI) MERCK & CO INC. PR (OYNY) UNIV NEW NEW YORK STATE. PI MAND P, Warmke JW. PI MAND P, Warmke JW. BN WIJ Se-259828/26. PT Co-expression of voltage-activated cation channel alpha and beta pr sub-units - esp. para and tipE sub-units of Drosophila voltage PT Sub-units - esp. para and tipE sub-units of Drosophila voltage PT Sub-units - esp. para and tipE sub-units of Drosophila voltage PT Co-expression of voltage-activated cation potential that underlies Co-expression of voltage-activated sodium channel (VASC), a protein responsible for activated sodium channel protein in biologically active form PS Claim 19: paga 36.40; 52pp; Engalish. CC A full-length cDNA clone (T19986) codes for the Drosophila para voltage-activated sodium channel (VASC), a protein responsible for the fast depolarising phase of the action potential that underlies CC the fast depolarising phase of the action potential that underlies CC of the para VASC requires the Co-expression of the para ApRC on be used community of the gene. CC ob PCR amplification using primers (See also 718987-92) based on a published para sequence. Recombinant host cells (E-coli, yeast community in the solate para VASC in biologically active form. Antisense CC constructs can block expression of the gene 1702 G; 1582 T; Query Match DATE OF CAST AND CONDERSOR CONDE	dear committee too.co., fied. No. o
######################################	: 188442 seqs, b8020449 bases x cessing: Minimum Match 0%	

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atches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 tctagacgttggccgcatagacaatgacagaagattccgatcgat	<pre>####################################</pre>	121 ctgaacatgaaaagcagaaggagctggaaagaaagaagccgagggagagggggggg	181 atggtcgcaagaaaaaacaaaagaaatccgatatgatgatgacgaggacgaggatgaaggtc 240 	241 cacaaccggatcctacacttgaacagggtgtgccaatacctgttcgattgcagggcagct 300 	301 tecegeoggaattggcetecaetectetegaggatategatecetaetaeggaatgtae 360 	361 tgacattcgtagttgtaagcaaaggaaaagatattttcgcttttctgcatcaaagcaa 420 	421 tgtggatgtcgatccattcaatccgatacgtcgtgtggccatttacattctagtgcatc 480	481 cattattttcctattcatcatcaccacaattctcgtcaactgcatcctgatgataatgc 540	541 cgacaacgcccacggttgagtccactgagtgatattcaccggaatctacacatttgaat 600 	601 cagctgttaaagtgatggcacgaggtttcattttatgcccgtttacgtatcttagagatg 660 	661 catggaattggctggacttcgtagtaatagctttagcttatgtgaccatgggtatagatt 720 	721 taggtaatctagcagccctgcgaacgtttagggtgctgcgagcgcttaaaaccgtagcca 780 	781 ttgtgccaggcttgaagaccatcgtcggcgcgtcatcgaatcggtgaagaatctgcgcg 840 	841 atgtgattatcctgaccatgttctccctgtcggtgttcgcgttgatgggcctacagatct 900 	901 atatgggcgtgctcaccgagaagtgcatcaagaagttcccgctggacggttcctggggca 960 	961 atctgaccgacgagaactgggactatcacaatcgcaatagctccaattggtattccgagg 1020 	1021 acgaggcatctcatttccgttatgcggcaatatatccggtgcggggcaatgcgacgacg 1080
Ma Db Qy	g &	g vò	g o	g S	Db Qy	g ö	g &	g &	qa Vo	da yo	do yo	g vo	g o	g ov	g &	oy Oy	g %

cgaatgccgtcaccccgatgtccgaagagaatggggccatcatagtgcccgtgtactatg attaogtgtgcctgcagggtttggtccgaatccgaattatggctacaccagcttcgatt tettectaggtteattetatettgtgaatttgattttggecattgttgceatgtegtatg g 07 09 g g δŽ ద δ g ò g ŏ g δŽ ò g g g οχ δy В δy g δ Db Qy 엄 δ qq δ g οy δ QΥ δ,

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43	321 TCGTCGTTAATGCGCTGGTACAAGCTATACCGTCCATCTTCAATGTGCTATTGGTGTGT 4380	5
43	381 taatattttggctaatttttgccataatgggtgtacagctttttgctggaaatatttta 4440 	i ö
44		g &
45	501 gcgagagcgagaactacacgtgggtgaattcagcaatgaattcgatcatgtaggtaacg 456 foll gcgagagcgagaactacacgtgggtgaattcagcaatgaattcgatcatgtaggtaacg 456 foll fillillillillillillillillillillillillill	DP VA
	561 cytatotytycctttccaagtgcaccttctcaaagggatacaaaccatgaaggg 462	g 8
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                                                                                                                                                         Mono-specific antibodies to voltage-activated cation channel - also new cation channel DNA, useful for identifying channel modulators, potentially useful partic. as insecticide and neuroprotective
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                               15-0CT-1996 (first entry)
Drosophila para voltage-activated sodium channel cDNA.
Para voltage-activated sodium channel; cation channel; insectic arachnicide; pesticide; neuroprotective; ischaemia; antagonist; therapy; monoclonal antibody; ss.
Drosophila melanogaster.
W09614660-A1.
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Pred. No. 0.00e+00;
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10-NOV-1994; US-338702.
(MERI) MERCK & CO INC.
Van Der Ploeg LHT, Warmke JW;
WPI; 96-259563/26.
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Similarity 100.0%;
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Claim 8: Fig lar.In; 39pp; English.

The cDNA is derived from 3 overlapping cDNA clones, designated are consisted from 5 overlapping cDNA clones, designated plasmid pRH3-1 (ATCC 67885), plasmid pRH4-23 (ATCC 67886) and plasmid pRH4-31 (ATCC 67887). A virus/circular DNA plasmid vector comprising the CDNA may be transformed or transfected into prokaryote/eukaryote host cell, and the resulting recombinant sodium channel protein has various therapeutic, diagnostic and prognostic uses. It may also be used to develop more effective antiarrythmic, sequence 7555 BP; 1577 A; 2309 C; 2103 G; 1566 T;
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081328;
08-3328;
Cardiac sodium channel protein coding sequence.
Sodium channel protein; ds; therapeutic; diagnostic; prognostic; antiarrythmic; cardialic; cardialic; cardialic; preserved.
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                             cttccgggtcatccgtctggccaggatcggccgcatcctcaggctgatccgcggagccaa
                                                                          GCTCCGAGTGGTGCGTGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTGAAGGGAGCCAA
                                                                                             GGGCATTCGGACACTGCTCTTCGCGTTGGCCATGTCGCCGGCCCTGTTCAACATCTG
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                    ctccattgttggcactgtcctccgacatcatccagaagtacttcttctcccgacact
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10-JAN-1991 (first entry)
Cardiac sodium channel gene.
Rat; arrhythmia; ss.
Rattus rattus.
W09009391-A.
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Q05831 standard; cDNA; 7555
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13-FEB-1989; US-310330.
(ARCH-) ARCH DEV CORP.
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P-PSDB; R06584.
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Claim 7; Fig 1; 65pp; English.

The sequence is derived from 3 overlapping clones, pRH3-1, pRH4-23 and pRH4-31.

The sequence is derived from 3 overlapping clones, pRH3-1, pRH4-23 and pRH4-31.

The clones were isolated from a cDNA library in the lambda Zap vector prepd. from mRNA obtd. from newborn rat hearts using rebrain II cDNA probe. The isolated DNA can be used to screen a brain II cDNA probe. The isolated DNA can be used to screen a brainlar human derived cardiac cDNA library for the corresponding human gene. Proteins and prognostic applications of the DNA have diagnostic therapeutic, and prognostic applications.

Sequence 7555 BP; 1576 A; 2314 C; 2101 G; 1564 T;
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                                                                                                                                                                                                                                                                                                          Length 7555;
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Pred. No. 2.00e-215;
0; Mismatches 650; Indels
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Best Local Similarity 63.3%;
Matches 1174; Conservative
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T30192 standard; cDNA; 3033 BP.
T30192,
T5-027-1996 (first entry)
Peripheral nervous system; sodium channel peptide-1 alpha-subunit gene.
Rat; peripheral nervous system; sodium channel; PN1; PC12; PKI-4;
CITTGAAATAGTAACCGATAAGAAATTCGATATAATCATTATGTTATTCATTGGTCTGAA 4963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgaccoggaggccacccagttcattgagtatctggccctgtccgactttgcagatgcctt
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                                        CTATCTCAATGCGATATTCGTAGTTATTTTCAGTTCCGAATGTCTATTAAAAATATTCGC
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Claim 2; Fig 7; 80pp; English.

The sequence encodes repeat domain-II of a rat peripheral nervous system sodium channel peptide-1 alpha-subunit (PNI), with sodium channel activity, and has been isolated from a rat PCI2 subclone of PNI-4 cell culture, expressing high levels of CAMP-dependent protein-kinase-inhibitor. A CDNA library has been screened with primers 730196-97, and the product has been used as a probe to re-screen the library to isolate this sequence. The full-length capen in 730193. A probe derived from the sequence may be used in differential tissue expression studies. The peptide may be used to isolate sodium-agonists and sodium-antagonists for use as an algesise, hypotensives, antiinflammatoories, and in therapy of sodium channel associated pathology or trauma, e.g. neurological disorders. The DNA (in sense or antisense orientation) may be used
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D 77-MX-1996.

D 77-MX-1995.

WR 02-NOV-1995; U14251.

PR 07-UN-1995; U5-482401.

PR 07-UN-1995; US-482401.

PA (TROP) TROPHIX PHARM INC.

PA (UNIV ) UNIV NEW YORK STATE RES FOUND.

PI Borden LA, Halegoua S, Mandel G;

DR WPI; 96-221547/25.

DR WPI; 96-29638.

PFSDB; R99638.

PT Nucleic acid encoding peripheral nervous system specific sodium nucleic acid encoding specific sodium nucleic acid specific sodium nucleic acid specific sodium nucleic specific sodium nucleic specific sodium nucleic 
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sodium-agonist; sodium-antagonist; drug screening; analgesic; hypotensive; antiinflammatory; trauma; pain; neurological disorder; antisense; gene therapy; ss.
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Local Similarity 62.3%; Pred. No. 1.22e-192;
les 1210; Conservative 0; Mismatches 700; Indels 33;
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/note= "T30193 contains G at this position"
697..1665
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/note= "Probe used in differential tissue
expression studies"
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/note= "Binds primer T30196"
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/note= "Binds primer T30197"
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Peripheral nervous system, sodium channel peptide-1 alpha-subunit generic peripheral nervous system; sodium channel; PN1; PC12; PK1-4; sodium-agonist; sodium-agonist; drug screening; analgesic; hypotensive; antiinflammatory; trauma; pain; neurological disorder; antisense; gene therapy; ss.
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                                    aactttgagacttttggcaacagcatgatctgcttgttccaaatcaccacctctgccggc
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/note= "Probe used in differential tissue
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/note= "Fragment T30192 (claim
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'note= "Binds primer T30196"
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/product= Full-length PNI
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/note= "T30192 c
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/note= "Binds
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                                                                                                                Example 1; Fig 9; 80pp; English.

The sequence encodes a rat peripheral nervous system sodium channel peptide-1 alpha-subunit (PNI), with sodium channel activity, and has been isolated from a rat PCI2 subclone PKI-4 cell culture, capressing high levels of cAMP-dependent protein kinase-inhibitor.

A cDNA library has been screened with primers 730196-97, and the product has been used as a probe to re-screen the library to roduct has been used as a probe to re-screen the library to solate the fragment given in T30192. This has been used to isolate the full-length gene. A probe derived from the sequence may be used in differential tissue expression studies. The peptide may be used to isolate sodium-agonists and sodium-antagonists for use as an algesics, hypotensives, antilnflammatchies, and in therapy of sodium channel-associated pathology or trauma, e.g. neurological disorders. The DNA (in sense or antisense orientation) may be used
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                                    Borden LA, Halegoua S, Mandel G;
WPI: 96-221547/25.
P-PSDB; R99639.
Nucleic acid encoding peripheral nervous system specific sodium
channel peptide - useful for sodium channel-associated disease
                                                                                                                                                                                                                                                                                                                         1632 T;
                                                                                                                                                                                                                                                                                                                                                Score 312; DB 22; Length 6452;
Pred. No. 1.22e-192;
0; Mismatches 700; Indels 33;
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07.-UNN-1995; US-482401.
(TROP) TROPHIX PHARM INC.
(UXNY) UNIV NEW YORK STATE RES FOUND.
Borden LA, Halegoua S, Mandel G;
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Best Local Similarity 62.3%;
Matches 1210; Conservative
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The sequence encodes a human peripheral nervous system sodium channel peptide-1 alpha-subunit (PNIA), with sodium channel activity. A probe has been isolated by PCR from a human peripheral nervous system cDNA library, using probes derived from the rat PNI protein sequence (R9658-39), and has been used to screen a human dorsal root ganglion cDNA library, to give the full-length sequence, using PCR primers 730198-99 and T18167. A related sequence (730195) has also been isolated. The sodium channel peptide may be used to isolate sodium agonists and sodium-intagonists for use as analgesics, hypotensives, antiinflammatories, and in therapy of sodium channel-associated pathology or trauma, e.g. neurological disorders. The DNA (in sense or antisense orientation) may be used
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                                                                 5826 AAGTACAAGATCATATCGATGGACATACCCATCTGTCGCGGGGGGGCTCATGTACTGCTGCGGG
                          5706 GACATGTACTATGAGATCTGGCAGCAATTCGATCCGGAGGGCACCCAGTACATACGCTAT
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                                                                                                            aaagtccagctcattgccatggacctgcccatggtgagtggagaccgcatccactgcctg
                                                                                                                                                                                                                                                                            25-OCT-1996 (first entry)
Peripheral nervous system sodium channel peptide-1 alpha-subunit
Human; peripheral nervous system; sodium channel; PNIA;
dorsal root ganglion; sodium-agonist; sodium-antagonist;
drug soreening; analgesic; hypotensive; antiinflammatory; trauma;
pain; neurological disorder; antisense; gene therapy; ss.
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Pred. No. 8.52e-190;
0; Mismatches 713; Indels 35;
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/product= PN1A protein
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07-JUN-1995; US-482401.
(TROP-) TROPHIX PHARM INC.
(UNIX ) UNIV NEW YORK STATE RES FOUND.
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WPI; 96-251547/2
P-PSDB; R99640.
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Peripheral nervous system sodium channel peptide-1 alpha-subunit grammen; peripheral nervous system; sodium channel; PNIB; dorsal root ganglion; sodium-agonist; sodium-antagonist; drug screening; analgesic; hypotensive; antinflammatory; trauma; pain; neurological disorder; antisense; gene therapy; ss.
                                                                                                                                      cttaacagtaagccacccgactgtgacccaaaaaaagttcatcctggaagttcagttgaa
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                                                                                                                                                                                                                                                                                     The sequence encodes a human peripheral nervous system sodium channel peptide-1 alpha-subunit (PNIB), with sodium channel activity. A probe has been isolated by PCR from a human peripheral nervous system cDNA library, using probes derived from the rat PNI protein sequence (R99638-39), and has been used to screen a human dorsal root ganglion cDNA library, to give the full-length sequence, using PCR primers T30198-99 and T18167. A related sequence (T30194) has also been isolated. The sodium channel peptide may be used to isolate sodium-agonists and sodium antagonists for use as analgesics, hypotensives, antinflammatories, and in therapy of sodium channel-associated pathology or trauma, e.g. neurological disorders. The DNA (in sense or antisense orientation) may be used
                                                                                                                                              WPI; 96-251547/2>.
P-SDB: R99641.
Nucleic acid encoding peripheral nervous system specific sodium
Annuel peptide - useful for sodium channel-associated disease or
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02-NOV-1995; U14251.
02-NOV-1994; US-334029.
07-JUN-1995; US-482401.
(TROP-) TROPHIX PHARM INC.
(UNIX ) UNIV NEW YORK STATE RES FOUND.
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Matches 1231; Conservative
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treatment of pain

Claim 9; Page 50-58; 128pp; English.

The sequences given in T77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulsest along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in gila, muscle or the neurons of the (para)sympathetic, enteric or central nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia.

Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T;
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CDNA encoding wild type rat DRG (SNS-B).

Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin; modulator; impulse; sensory neuron; acute pain; chronic pain; neuropathic pain; glia; muscle; parasympathetic nervous system; enteric nervous system; central nervous system; central nervous system; central ganglia; so.
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16-7017-1996; G01523.
28-7017-1995; G8-013180.
(UNLO ) UNLY COLLEGE LONDON.
Akopian AN, Wood JN;
PP-SDB W21737.
New isolated mammalian sensory neuron sodium channel pi
to identify modulators of the sodium channel, partic.
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Pred. No. 2.83e-181;
0; Mismatches 486;
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Local Similarity 63.8%;
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177806 standard; CDNA; 6527 BP.
177806 standard; CDNA; 6527 BP.
177806.
09-0CT-1997 (first entry)
CDNA encoding variant rat DRG (SNS-B) #3.
modulator; impulse; sensory neuron; acute pain; chronic pain;
modulator; impulse; sensory neuron; acute pain; chronic pain;
entry pain; glia; muscle; parasympathetic nervous system;
enteric nervous system; central nervous system; dorsal root ganglia;
cranial ganglia; ss.
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Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxi, modulator; impulse; sensory neuron; acute pain; chronic pain; neuropathic pain; glia; muscle; parasympathetic nervous system; central nervous system; cranial ganglia; ss.
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  5091 agcttcgctaacgtcgtggacgaggccgcatcgacgacatgttcaacttcaagaccttt
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                                                                                                  5193 TCGCCGACCCTGCTCCGAGTGGTGCGTGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTG
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T77805 09-0CT-1997 (first entry)
CDNA encoding variant rat DRG (SNS-B) #2.
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The sequences given in T77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the (paralsympathetic, enteric or central nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia. This sequence contains 12 nucleotide differences to the wildtype rat DRG(SNS-B) (see also 777803) causing nine amino acid changes.

Sequence 6527 BP; 1542 A; 1863 C; 1663 G; 1459 T;
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                                                                                                                                                                                                   New isolated mammalian sensory neuron sodium channel protein to identify modulators of the sodium channel, partic. for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6527;
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Pred. No. 2.83e-181;
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/note= "Addition
                                                                                                28-JUN-1995; GB-013180.
(UNLO ) UNIV COLLEGE LONDON.
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Similarity 63.8%;
900; Conservative
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25-JUN-1996;
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25-JUN-1996; G01523.
28-JUN-1995; GB-013180.
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                                                                                            treatment of pain 1978; 128pp; English.

Claim 9: Page 69-78; 128pp; English.

The sequences given in T77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the codium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the (para)sympathetic, enteric or central nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia. This sequence encodes a 2132 amino acid protein that contains a 176 amino acid repeat inserted after amino acid 585 of wildtype rat DRG(SNS-B)
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                                                                                                                                                                                                                                                                                         1593 T;
                                                                                                                                                                                                                                                                                                              Score 296; DB 32; Length 7052;
Pred. No. 2.83e-181;
0; Mismatches 486; Indels 18;
                                                                                      for the
                                                                       New isolated mammalian sensory neuron sodium channel protein to identify modulators of the sodium channel, partic. for the
                                                                                                                                                                                                                                                                                         1795 G;
                                                                                                                                                                                                                                                                                         2009 C;
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                        UNIV COLLEGE LONDON
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Local Similarity 63.8%;
les 890; Conservative
           GB-013180
                                    Wood JN;
                                                                                                                                                                                                                                                                                        7052 BP;
                                    Akopian AN, Wood wPI; 97-100165/09.
P-PSDB; W21739.
                                                                                                                                                                                                                                                                                         Sequence
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CDNA encoding variant rat DRG (SNS-B) #1.

CDNA encoding variant rat DRG (SNS-B) #1.

Mat, sensory neuron sodium channel protein; insensitive; tetrodotoxin; modulator; impulse; sensory neuron; acute pain; chronic pain; miscle; parasympathetic nervous system; central nervous system; central nervous system; dorsal root ganglia; cranial ganglia; ss.

Kattus rattus.

Location/Qualifiers

S61..2126
                                                                                                                                                           TATCCGGGCAATTGTGGTTCAGCGACCGTTGGAATAACGTTTCTCCTCTCATACCTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgggagaagttcgacccggaggccacccagttcattgcttttctgccttctggattc
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TCGCCGACCCTGCTCCGAGTGGTGCGTGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTG
                                                       AAGGAGCCAAGGGCATTCGGACACTGCTTCGCGTTGGCCATGTCGCTGCCGGCCCTG
                                                                                                                                                                                                                                                                       agettegetaaegtegtggaegaggeeggeategaegaeatgtteaaetteaagaeettt
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1451

1511

5795 1631

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aacacggggcottcctactgcgaccccaactgcccaacagcaacggctcccgggggaac 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q71202 standard; DNA; 2308 BP.
Q71202 d71202 standard; DNA; 2308 BP.
Q71202 d71203 d71204 d71205 (first entry)
scd131, a subclone of hscpl, encodes a non-dipteran sodium channel.
non-dipteran sodium channel; lepidoptera; insecticide; sensitivity;
target site; pyrethroids; marker; resistance; probes; detection;
PCR; polymerase chain reaction; Heliothis; degenerate;
Drosophila melanogaster; homologue; hspc1; para locus; scd13; ss.
                                                                                                                                                                                                                                                                                                                                                             ttggtccccggggataagatccactgtctggacatcctttttgccttcacaaagaacgtc
                            5505 AAT -- GAGGAAGC -- - A-TGCGATCC -- ACCCGAC - AGCGACAAAGGCTATCCGGGCAAT
                                                                         1392 atcgtggtcaacatgtacatcgcagtgattctggagaacttcaacgtagccaccgaggag
                                                                                                                                                                                      5796 GAGCCCCCCCTGCAGATCCACAAACCGAACAAGATACAAGATCATATCGATGGACATACCC
                                                         tgcgggagcccggcggtgggcatcatcttctcaccacctacatcatctcctc
                                                                                                                                                                      1452 agcacggagcccctgagcgaggacgacttcgacatgttctatgagacctgggagagttc
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/note= "end of putative intron"
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/note= "putative intron"
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                                                                            The sequences given in T7803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel. Blockers of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the dorsal root ganglia or cranial ganglia. This the neurons of the dorsal root ganglia or cranial ganglia. This chequence represents bases 4512-6524 of wildtype rat DRG(SNS-B) (see also 177803), and encodes residues 1437-1957 of the mature protein.
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                                                                                                                                                                                                                                                                                                 Score 231; DB 32; Length 2573;
Pred. No. 2.36e-135;
0; Mismatches 403; Indels 15;
                                          protein for the
                                       New isolated mammalian sensory neuron sodium channel p
to identify modulators of the sodium channel, partic.
                                                                                                                                                                                                                                                                                                 Query Match 3.5%;
Best Local Similarity 63.4%;
Matches 724; Conservative
Wood JN;
           WPI; 97-100165/09.
P-PSDB; W21738.
                                                                  treatment of pain
 Akopian
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Lagangle 2: Fig1; 32pp; English.

Q71200-202 are the DNA sequences of the subclones, scd61, scd72, and. scd131 respectively, from the genomic clone "hscp1". The hscp1 clone is approximately 8000 bp and encodes a sodium channel protein. The clone was isolated from a pyrethroid resistant PEG-87 library. The non-dipteran sodium channel is thought to be the target site for sensitivity to a variety of different insecticides and is useful as a marker for target insensitive insecticide resistance. Q71198-99 are degenerate primers used to isolate hscp1. The primers are based on an homologous sequence of the Drosophila para locus, in particular a portion of an exon in the fourth transmembrane domain of the a-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5149 TCTTAGGTCTTGTACTTAGCGATATTATCGAGAAGTACTTCGTGTCGCCGACCCTGCTCC 5208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5389 AGGAGAAGAGGGGCATTAAACGACGTCTACAAGACCTTTAGGCCAGAGAGATGATCC 5448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1602 tctcaggttttggtattgagtgatattatagaaaaatattttgtgtcacccacgttactga 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5209 GAGTGGTGCGTGTGGCGAAAGTGGGCCGTGTCCTTCGACTGGTGAAGGGAGCCAAGGGCA 5268
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/note= "putative exon"
1913..2095
/*tag= "kag= "putative intron"
2096..2308
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/note= "any of T,C,G or
2158
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                                                   *tag= 1
note= "putative exon"
70..2308
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Black BC, Kreitman M, Taylor M;
WPI; 94-272316/34.
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"either
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larity 78.5%; Conservative
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107
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/note=
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24-DEC-1993; 112445.
30-DEC-1992; US-998289.
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RESULT 14 ID Q71200 standard; DNA; 2416 BP.

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Example 2; Fig 1; 32pp; English.

O/1200-202 are the DNA sequences of the subclones, scd61, scd72, and scd131 respectively, from the genomic clone "hscp1". The hscp1 clone is approximately 8000 bp and encodes a sodium channel protein. The clone was isolated from a pyrethroid resistant PEG-87 library. The cond-tipreran sodium channel is thought to be the target site for sensitivity to a variety of different insecticides and is useful as marker for target insensitive insecticide resistance. Q71198-99 are degenerate primers used to isolate hscp1. The primers are based on an homologous sequence of the Drosophila para locus, in particular a portion of an exon in the fourth transmembrane domain of the arsubunit. Sequence 2416 BP; 709 A; 436 C; 487 G; 756 T;
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12-MAY-1995 (first entry) sodél, a subclone of hscpl, encodes a non-dipteran sodium channel. non-dipteran sodium channel: lepidoptera; insecticide; sensitivity; target site; pyrethroids; marker; resistance; probes; detection; sense primer; PCR; polymerase chain reaction; Heliothis; degenerate; Drosophila melanogaster; homologue; hspcl; para locus; scd61; ss. Heliothis virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/note= "HSC 3455+ ("abelard") (numbering based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detecting insecticide sensitivity or resistance in insects, pref.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 41; Indels
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440..522
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/note= "start of intron"
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/note= "end of intron"
298..441
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N81164 standard; DNA; 204
N81164;
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796..882
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523..795
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30-DEC-1992; US-9982
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ID N8
AC N8
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A COURTED STATEMENT OF THE STATEMENT OF ST
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 1; Length 204; Pred. No. 1.33e-13; 63; Mismatches 36; Indels
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/*tag= a
/function=multiple cloning site
187..204
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 C;
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 17.2%;
Matches 21; Conservative
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30-MAR-1988; 105163
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Search completed: Sun Sep 13 07:20:05 1998 Job time : 1113 secs. || 5842 CG 5843

cg 197

196

5782 ICCTGGACGTACTGGAGCCCCGCTGCAGATCCACAAACCGAACAAGTACAAGTACAAGTTCATAT 5841

136 yvybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvchccgat 195

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:|::|| |:::|| |:::|| 5722 TCTGGCAGCACTACAGTACATACGCTATGATCAGCTGTCCGAAT 5781 78 dchvgccgymrttt-hhyrrmrbnvyrdynrsdaaawyc-cyrrsvkydccynachhddh 135

Gaps

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- n.a. database search, using Smith-Waterman algorithm

л. В.

Sun Sep 13 04:30:04 1998; MasPar time 6599.57 Seconds 1382.167 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-554-424-7 (1-6513) from US08554424.seq 6513 Title: Description: Perfect Score: N.A. Sequence: Comp:

1 TCTAGACGTTGGCCGCATAG......AGGGGGGTATTAGCTCTAGA 6513
AGATCTGCAACGGGGTATC......TGGGCTCATAATCGAGATCT

TABLE default Scoring table:

Dbase 0; Query 0 Gap 6 Nmatch STD

1832099 segs, 700269816 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-est55 Database:

1:em_est10 2:em_est11 genbank-est107 Database:

3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13 8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17 12:gb_est18 13:gb_est19 14:gb_est2 15:gb_est20 16:gb_est2 15:gb_est2 15:gb_est2 20:gb_est4 21:gb_est5 22:gb_est6 23:gb_est7 24:gb_est8 25:gb_est9 26:gb_est8

Mean 12.798; Variance 2.257; scale 5.669 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.16e-198	4.89e-192	4.27e-144	5.18e-127	1.01e-97	1.15e-95	1.93e-83	1.68e-67	1.92e-71	2.07e-77	2.00e-73	1.19e-61	1.36e-63
Description	H. sapiens partial cDN	ms53e02.rl Life Tech m	vb09f10.rl Soares mous	F.rubripes GSS sequenc	ve83f11.rl Soares mous	am76b09.sl Stratagene	97SN1787 Rice Immature	EST70140 T-cell lympho	97SN1787 Rice Immature	vz09a09.rl Stratagene	HL08049.5prime HL Dros	97SN1784 Rice Immature	97SN1784 Rice Immature
1	HSC2HD061	AA183990	AA272867	FR0002753	AA427267	AA984063	AA754459	AA360938	AA754459	AA914778	AA699257	AA754458	AA754458
DB	21	24	25	56	2	18	13	4	13	16	11	13	13
å Query Match Length DB	343	529	594	619	413	206	252	214	252	328	573	247	247
Query Match	1.9	1.9	1.5	1.4	1.2	1.2	1.1	1.0	1.0	1.0	1.0	6.0	6.0
Score	124	121	66	91	77	-16	70	62	64	29	65	29	9
Result No.	ч	7	m	4	S	9	7	œ	σ	10	11	12	13
Res						υ	ပ	υ					ပ

Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA

Primer: M13_reverse
CDNA sequence colinear to mRNA
Stretch_removed: nothing
Normalization_method: Bento Soares, P.N.A.S. 91:9228-9232(1994):

Sequencing_method: single read, full automatic; Primer: M13_reverse

4 9 0 8 430 16 AAA11881 am34211.5 Soares NFL 8 90e- 6 0 0 8 437 16 FR000275 Frubribes GSS sequenc 129e- 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	49 0.8 330 16 AA893381 ama4cl13 s2 Soares NRL
10. 8 435 16 AA813881 am340.11.81 Soarses NFL 8.908-43	49 0.8 4330 16 AA013881 ama14.2.13 Soares.NFL 8.90e-43 50 0.8 477 56 FROMO2729 F.TUDTIPES GSS SEQUENC 1.39e-44 51 0.7 4272 16 AA014.661 2.39e-44 52 0.7 407 68 16 FROMO2750 F.TUDTIPES GSS SEQUENC 1.66e-35 53 0.7 407 26 FROMO2751 F.TUDTIPES GSS SEQUENC 1.66e-35 54 0.7 619 26 FROMO2751 F.TUDTIPES GSS SEQUENC 1.66e-35 55 0.7 607 26 FROMO2751 F.TUDTIPES GSS SEQUENC 1.66e-35 60 0.6 407 26 FROMO2751 F.TUDTIPES GSS SEQUENC 1.66e-35 60 0.6 407 26 FROMO2751 F.TUDTIPES GSS SEQUENC 1.66e-35 60 0.6 541 17 AA059928 v-200404 1.5 Soares tota 6.86e-27 60 0.6 541 17 AA059928 v-200404 1.5 Soares tota 6.86e-27 60 0.6 541 17 AA059928 v-200404 1.5 Soares mous 2.56e-27 60 0.6 588 18 AA0687 V-200404 1.5 Soares tota 6.86e-27 60 0.6 588 18 AA0687 V-200404 1.5 Soares tota 2.71e-20 60 0.6 588 18 AA0687 V-200404 1.5 Soares tota 2.71e-20 60 0.6 541 17 AA059928 v-200404 1.5 Soares mous 2.56e-20 60 0.6 541 17 AA059928 v-200404 1.5 Soares mous 2.56e-20 60 0.6 588 18 AA0687 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares mous 2.56e-20 60 0.6 540 7 AR0489 V-200404 1.5 Soares Mous 2.5 Soares Mous 2.5 Soares Mous 2.5 Soares V-200404 1.5 Soares V-200404 1.5 Soares V-200404 1.
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49 0.8 430 16 AA8913881 om21h12.s2 Soares_NFL_ 8.90e- 43 0.8 437 26 FR0002729 F.rubripes GSS sequenc 1.20e- 43 0.7 225 16 AA214661 zq89e09.r1 Stratagene 4.83e- 44 0.7 225 16 FR000275 F.rubripes GSS sequenc 1.46e- 45 0.7 404 17 EST1984 Normalized r 4.83e- 45 0.7 404 25 FR000273 F.rubripes GSS sequenc 1.46e- 45 0.7 407 26 FR000273 F.rubripes GSS sequenc 1.46e- 46 0.7 6 FR000279 F.rubripes GSS sequenc 1.46e- 47 0.6 407 26 FR000279 F.rubripes GSS sequenc 1.46e- 48 0.6 541 17 AA520400 ae57d3.s1 Stratagene 6.86e- 49 0.6 541 17 AA598592 W.W5803.s1 Soares mous 2.63e- 40 0.6 541 17 AA598592 W.W5803.s1 Soares mous 2.63e- 40 0.6 541 17 AA598592 W.W5803.s1 Soares mous 2.63e- 42 0.6 541 17 AA598592 W.W5803.s1 Soares mous 2.63e- 43 0.5 541 17 AA598592 C.RUBripes GSS sequenc 2.63e- 44 0.6 541 17 AA598592 W.W5803.s1 Soares mous 2.63e- 45 0.6 541 17 AA598592 W.W5803.s1 Soares mous 2.63e- 45 0.6 541 17 AA598592 W.W5803.s1 Soares mous 2.63e- 46 0.6 541 17 AA550400 EST9641 Teatis I Homo 3.93e- 47 0.6 541 17 AA550400 F.RUBROOP T. Cruzi epim 3.93e- 48 0.5 541 2 AA112441 zm27601.r1 Stratagene 1.06e- 48 0.5 443 22 HSZ7839 H.sapiens mRNA, expres 1.39e- 47 0.5 643 24 AA306559 EST377527 JULKAT T-CEI 1.06e- 48 0.5 532 7 AA445889 SWAMCA17285K Brugia ma 3.93e- 47 0.5 532 7 AA445889 SWAMCA17285K Brugia ma 3.93e- 47 0.5 532 7 AA445889 SWAMCA17285K Brugia ma 3.93e- 47 0.5 532 1 WZ7487 HUGH To spiens mRNA, expres 3.93e- 47 0.5 532 1 WZ7487 HUGH To spiens mRNA, expres 3.93e- 47 0.5 532 1 WZ7487 HUGH To spiens mRNA, expres 3.93e- 47 0.5 532 1 WZ0659 SWAMCA17285K Brugia ma 3.93e- 47 0.5 532 1 WZ7487 HUGH To spiens mRNA, expres 3.93e- 47 0.5 532 1 WZ7487 HUGH To spiens mRNA, expres 3.93e- 47 0.5 532 1 WZ7487 HUGH To spiens mRNA, expres 3.93e- 47 0.5 532 1 WZ7487 HUGH To spiens mRNA, expres 3.93e- 47 0.5 532 1 WZ7487 HUGH To spiens mRNA, expres 3.93e- 47 0.5 5275 12 AF034173 HUGH Sequence; clone c-2hd06, mRNA sequence	49 0.8 330 16 AA913881 om21hi2.s2 Soares_NFL_ 8.90e- 49 0.8 435 16 AA885211 am34c11.s1 Soares NFL 8.90e- 45 0.7 225 16 AA214661 zq89e09.r1 Stratagene 1.83e- 45 0.7 225 16 AA214661 zq89e09.r1 Stratagene 1.46e- 45 0.7 386 26 FR0002750 F.rubripes GSS sequenc 1.46e- 45 0.7 604 26 FR000273 F.rubripes GSS sequenc 1.46e- 45 0.7 604 26 FR000273 F.rubripes GSS sequenc 1.46e- 46 0.6 267 10 AA620400 ae57d03.s1 Stratagene 2.63e- 47 0.6 407 26 FR0002725 F.rubripes GSS sequenc 2.63e- 48 0.6 546 7 AA44697 zw90c04.s1 Soares tota 6.86e- 49 7 AA44697 zw90c04.s1 Soares tota 6.86e- 40 0.6 546 7 AA44697 zw90c04.s1 Soares tota 2.71e- 40 0.6 546 7 AA44697 zw90c04.s1 Soares tota 2.71e- 40 0.6 546 7 AA44697 zw90c04.s1 Soares tota 2.71e- 40 0.6 546 7 AA44697 zw90c04.s1 Soares tota 3.93e- 40 0.5 546 7 AA44697 zw90c04.s1 Soares tota 2.71e- 40 0.6 2275 12 AF034173 mr75b01.r1 Stratagene 1.06e- 40 0.5 269 16 AA867902 TENS0009 T. cruz1 epim 3.93e- 40 0.5 384 12 AA112441 zm27902.r1 Stratagene 1.06e- 40 0.5 340 AA306559 EST177527 Jurkat T-cel 1.06e- 41 0.5 540 AA306559 EST177527 Jurkat T-cel 1.06e- 41 0.5 540 AA446889 SWAMCA17288K Bruja ma 3.93e- 41 0.5 532 TRAA5889 SWAMCA1728K Bruja ma 3.93e- 41 0.5 532 TRAA5899 SWAMCA1738K Bruja ma 3.93e- 41 0.5 532 TRAA5899 SWAMCA1738K Bruja ma 3.93e- 41 0.5 532 TRAA5899 SWAMCA1738K Bruja ma 3.93e- 41 0.5 532 TRAA589 SWAMCA1738K Bruja ma 3.93e- 4
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14 49 0.8 330 16 AA911881 om21712.52 Soares_NFL_ 8.90e- 15 49 0.8 437 26 FR0002729 F.rubripes GSS sequenc 1.29e- 17 43 0.7 225 16 AA214661 zq89e09.r1 Stratagene 4.83e- 18 45 0.7 225 16 FR0002750 F.rubripes GSS sequenc 1.46e- 18 45 0.7 404 17 AA94291 EST198470 Normalized r 4.83e- 20 45 0.7 404 26 FR0002732 F.rubripes GSS sequenc 1.46e- 21 45 0.7 619 26 FR0002732 F.rubripes GSS sequenc 1.46e- 22 45 0.7 619 26 FR0002759 F.rubripes GSS sequenc 1.46e- 23 40 0.6 407 6 FR0002759 F.rubripes GSS sequenc 1.46e- 24 42 0.6 499 7 AA446879 zw96004.s1 Soares mous 2.63e- 25 40 0.6 649 7 AA44689 vw56004.s1 Soares mous 2.63e- 26 42 0.6 541 17 AA959928 vw56004.s1 Soares mous 2.63e- 27 36 0.6 541 17 AA95929 vw56004.s1 Soares mous 2.63e- 28 39 0.6 541 17 AA95809 vw56004.s1 Soares mous 2.63e- 29 42 0.6 619 26 FR000275 F.rubripes GSS sequenc 2.63e- 29 42 0.6 619 26 FR000275 F.rubripes GSS sequenc 2.63e- 31 35 0.5 541 17 AA95809 vw56004.s1 Soares mous 3.09e- 32 44 0.5 541 17 AA95809 vw56004.s1 Soares mous 3.09e- 33 34 0.5 55 22 HSZ7830 vb66.c0 1.1 Stratagene 1.06e- 34 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 35 0.5 413 4 AA306559 H.sapiens mRNA, expres 3.93e- 36 0.5 541 2 AA144007 mr75b01.r1 Stratagene 1.06e- 38 0.5 413 4 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 541 14 AA306559 H.sapiens mRNA, expres 3.93e- 44 0.5 542 142 148 148 148 148 148 148 148 148 148 148	14 49 0.8 330 16 AA913881 am34cli.s. Soares_NFL 8.90e-15 16 50 0.8 435 16 AA882211 am34cli.s. Soares NFL 8.90e-17 225 16 AA214661 xq89e09: I Stratagene 1.29e-18 225 16 AA214661 xq89e09: I Stratagene 1.46e-18 22 0.7 404 7 AA942971 EST198470 Normalized 1.46e-18 22 45 0.7 404 7 AA942971 EST198470 Normalized 1.46e-18 22 45 0.7 404 25 FR000275 F.rubripes GSS sequenc 1.46e-18 22 45 0.7 604 26 FR000275 F.rubripes GSS sequenc 1.46e-18 22 40 0.6 267 0 AA620400 EST3081 Stratagene 1.46e-18 22 40 0.6 267 0 AA620400 EST3081 Stratagene 2.63e-18 22 40 0.6 24 20 24 20 25 24 20 26 24 20 26 24 20 26 24 20 26 24 20 26 24 20 26 24 20 26 24 20 26 24 20 25 24 25
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14 49 0.8 330 16 AA913881 om21712.52 Soares_NFL_ 8.90e- 15 49 0.8 437 26 FR0002721 am34cl1.s1 Soares NFL 1.29e- 16 0.8 437 26 FR0002721 am34cl1.s1 Soares NFL 1.29e- 18 45 0.7 225 16 AA214661 zq89e09.r1 Stratagene 4.83e- 19 43 0.7 404 17 AA94291 EST198470 Normalized r 4.83e- 20 45 0.7 404 26 FR0002732 F.rubripes GSS sequenc 1.46e- 21 45 0.7 619 26 FR0002759 F.rubripes GSS sequenc 1.46e- 22 45 0.7 619 26 FR0002759 F.rubripes GSS sequenc 1.46e- 23 40 0.6 407 26 FR0002759 F.rubripes GSS sequenc 1.46e- 24 42 0.6 409 7 AA446897 zw90c04.s1 Soares tota 6.86e- 25 40 0.6 541 17 AA559928 vw58903.s1 Stratagene 6.86e- 26 42 0.6 541 17 AA559928 vw58903.s1 Soares tota 2.71e- 27 36 0.6 546 7 AA446897 zw90c04.r1 Soares tota 2.71e- 28 39 0.6 546 7 AA446897 zw90c04.r1 Soares tota 2.71e- 28 30 0.6 546 7 AA446897 zw90c04.r1 Soares tota 2.71e- 29 42 0.6 6 19 26 FR0002754 F.rubripes GSS sequenc 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares tota 2.71e- 28 39 0.6 546 7 AA446897 zw90c04.r1 Soares tota 2.71e- 28 39 0.6 540 7 AA446897 zw90c04.r1 Soares tota 2.71e- 28 30 0.6 540 7 AA446897 zw90c04.r1 Soares tota 2.71e- 38 18 AA9485592 UcB1906.y1 Sugano mous 3.93e- 39 0.5 52 14 22443309 ub61c07.r1 Soares mous 3.93e- 31 35 0.5 52 14 22443090 T.rubripes GSS sequenc 3.93e- 31 34 0.5 52 14 AA1401 zm27902.r1 Stratagene 3.93e- 32 14 0.5 409 24 AA12441 zm27902.r1 Stratagene 3.93e- 33 34 0.5 413 AA365254 mr77501.r1 Stratagene 3.93e- 34 35 0.5 413 AA365254 mr77501.r1 Stratagene 3.93e- 34 0.5 413 CR002733 F.rubripes GSS sequenc 1.06e- 35 443 0.5 52 7 AA44889 SWAMAH17288K Brugia ma 3.93e- 34 0.5 52 7 W278389 W.saplens mRNA, expres 3.93e- 34 0.5 52 7 W278389 W.saplens mRNA, expres 3.93e- 34 0.5 52 7 W278389 W.saplens mRNA, expres 3.93e- 34 0.5 52 7 W278389 W.saplens mRNA, expres 3.93e- 34 0.5 52 7 W278389 W.saplens mRNA, expres 3.93e- 34 0.5 52 7 W278389 W.saplens mRNA, expres 3.93e- 34 0.5 52 7 W278389 W.saplens mRNA, expres 3.93e- 34 0.5 52 7 W278389 W.saplens mRNA, expres 3.93e- 35 70 70 70 70 70 70 70 70 70 70 70 70 70	14 49 0.8 330 16 AA913881 om21h12.52 Soares_NFL 15 49 0.8 435 16 AA885211 am34c11.51 Soares_NFL 16 50 0.8 435 16 AA885211 am34c11.51 Soares NFL 17 43 0.7 225 16 AA214661 zq89e09.r1 Stratagene 18 45 0.7 225 16 AA214661 Extibitions GSS sequenc 1.46e- 20 45 0.7 404 17 AA92971 Extibitions GSS sequenc 21 45 0.7 604 26 FR0002750 Frubripes GSS sequenc 22 45 0.7 604 26 FR0002751 Frubripes GSS sequenc 23 40 0.6 567 10 AA44878 Extibitions GSS sequenc 24 40 0.6 541 17 AA95928 Frubripes GSS sequenc 25 40 0.6 541 17 AA95929 Frubripes GSS sequenc 26 546 7 AA446878 zw90co4.s1 Soares tota 27 606 546 7 AA446878 zw90co4.s1 Soares tota 28 606 546 7 AA446878 zw90co4.s1 Soares tota 29 606 588 18 AA988592 UcB190cy1 Soares tota 20 619 26 FR0002754 Frubripes GSS sequenc 20 7 619 26 FR0002754 Frubripes GSS sequenc 20 8 8 8 AA986592 UcB190cy1 Soares tota 20 9 7 AA446878 zw90co4.s1 Soares tota 20 9 7 AA446878 zw90co4.s1 Soares tota 20 9 1 AA446878 zw90co4.s1 Soares tota 20 9 1 AA446878 zw90co4.s1 Soares tota 20 9 1 AA446878 zw90co4.s1 Soares tota 20 9 1
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14 49 0.8 330 16 AA813181 om21712.52 Soares_NFL_ 8.90e- 15 49 0.8 437 26 FR0002721 am34cl1.s1 Soares NFL 16 0.8 437 26 FR0002721 am34cl1.s1 Soares NFL 17 43 0.7 225 16 AA214661 zq89e09.r1 Stratagene 4.83e- 18 45 0.7 404 17 AA942921 Extrategene 5.85 sequenc 1.46e- 20 45 0.7 407 26 FR0002732 F.rubripes GSS sequenc 1.46e- 21 45 0.7 609 26 FR0002732 F.rubripes GSS sequenc 1.46e- 22 45 0.7 619 26 FR0002759 F.rubripes GSS sequenc 1.46e- 23 40 0.6 267 10 AA620400 ae57d03.s1 Stratagene 6.86e- 24 42 0.6 407 26 FR0002759 F.rubripes GSS sequenc 1.46e- 25 40 0.6 409 7 AA44689 vw58903.s1 Stratagene 6.86e- 26 42 0.6 541 17 AA959928 vw58903.s1 Soares tota 2.71e- 27 36 0.6 541 17 AA959928 vw58903.s1 Soares tota 2.71e- 28 39 0.6 544 17 AA446897 zw90c04.r1 Soares tota 2.71e- 29 42 0.6 619 26 FR0002754 F.rubripes GSS sequenc 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.29e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.29e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.39e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.39e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.39e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.39e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.39e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.39e- 29 42 0.6 541 17 AA959309 vb61c07.r1 Soares mous 3.39e- 20 575 12 AF278350 H.sapiens mRNA, expres 3.39e- 20 42 AA12441 zm27501.r1 Stratagene 3.93e- 21 40 0.5 541 4 AA144097 zm27601.r1 Stratagene 3.93e- 21 40 0.5 541 AA144097 zm27601.r1 Stratagene 3.93e- 21 40 0.5 541 AA144097 zm27601.r1 Stratagene 3.93e- 21 40 0.5 541 AA144097 zm27601.r1 Stratagene 3.93e- 21 41 AA306559 EST177527 Jurkat T-cel 1.06e- 21 41 41 AA306559 H.sapiens mRNA, expres 3.93e- 21 41 41 AA306559 H.sapiens partial cDN 3.93e- 21 41 24 52638 Sequenc 5.95e- 21 42 5268 Sequenc 5.95e- 22 443 72 EKSD0097 H.sapiens mRNA, expres 3.93e- 23 54 54 54 54 54 54 54 54 54 55 55 55 55	14 49 0.8 330 16 AA913881 om21h12.52 Soares_NFL_ 8.90e-15 0.8 435 16 AA885211 am34c11.51 Soares_NFL_ 8.90e-17 225 16 AA214661 zq89e09.r1 Strattgene 7.29e-17 225 16 AA214661 zq89e09.r1 Strattgene 7.29e-18 0.7 407 417 AA942971 Extibities GSS sequenc 1.46e-18 0.7 604 26 FR0002750 F.rubripes GSS sequenc 1.46e-18 0.7 604 26 FR0002751 F.rubripes GSS sequenc 1.46e-18 0.7 604 26 FR0002751 F.rubripes GSS sequenc 1.46e-19 26 FR0002752 F.rubripes GSS sequenc 1.46e-19 26 FR0002751 F.rubripes GSS sequenc 1.46e-19 26 FR0002752 F.rubripes GSS sequenc 1.46e-19 26 FR0002754 F.rubripes GSS sequenc 2.63e-19 26 FR0002755 F.rubripes GSS sequenc 2.63e-19 26 FR000275 F.rubripes GSS sequenc 2.63e-19 26 FSCF177527 F.rubripes GSS sequenc 2.63e-19 26 FSCF17
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14 49 0.8 330 16 AA913881 om21512.52 Soares_NFL_ 8.90e- 15 49 0.8 437 26 FR0002721 am34cl1.s1 Soares NFL 16 50 0.8 437 26 FR0002721 am34cl1.s1 Soares NFL 17 43 0.7 225 16 AA214661 zq89e09.r1 Stratagene 4.83e- 18 45 0.7 404 17 AA94291 EST198470 Normalized r 4.83e- 20 45 0.7 407 26 FR0002732 F.rubripes GSS sequenc 1.46e- 21 45 0.7 619 26 FR0002732 F.rubripes GSS sequenc 1.46e- 22 45 0.7 619 26 FR0002759 F.rubripes GSS sequenc 1.46e- 23 40 0.6 267 10 AA62040 ae57d03.s1 Stratagene 6.86e- 24 42 0.6 409 7 AA44689 zw9C004.s1 Soares tota 2.63e- 25 40 0.6 541 17 AA959928 vw58903.s1 Soares tota 2.63e- 26 42 0.6 541 17 AA959928 vw58903.s1 Soares tota 2.71e- 28 39 0.6 544 17 AA959928 vw58903.s1 Soares tota 2.71e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares tota 2.71e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.63e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.93e- 29 42 0.6 541 17 AA986590 rrbnipes GSS sequenc 2.94e- 20 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	14 49 0.8 330 16 AA913881 om21h12.52 Soares_NFL_ 8.90e-15 0.8 435 16 AA885211 am34c11.51 Soares_NFL 8.90e-17 225 16 AA214661 gag9e09.r1 Strattgener 1.29e-18 0.7 225 16 AA214661 gag9e09.r1 Strattgener 1.29e-18 0.7 225 16 AA214661 gag9e09.r1 Strattgener 1.46e-18 0.7 404 17 AA92971 gag9e09.r1 Strattgener 1.46e-18 0.7 604 26 FR0002750 F.rubripes GSS sequenc 1.46e-18 0.7 604 26 FR0002751 F.rubripes GSS sequenc 1.46e-18 0.7 604 26 FR0002751 F.rubripes GSS sequenc 1.46e-18 0.7 604 26 FR0002751 F.rubripes GSS sequenc 1.46e-18 0.6 67 10 AA620400 ae57403.s1 Strattgener 1.46e-19 26 FR0002755 F.rubripes GSS sequenc 1.46e-19 0.6 67 10 AA620400 ae57403.s1 Strattgener 1.46e-19 0.6 67 10 AA620400 ae57403.s1 Strattgener 1.66e-19 0.6 67 10 AA659028 F.rubripes GSS sequenc 2.63e-19 0.6 68 18 AA986592 gag90004.s1 Soares tota 2.71e-19 0.6 546 7 AA446878 zw90c04.s1 Soares tota 2.71e-19 0.6 546 7 AA446878 zw90c04.r1 Strattgener 1.06e-19 0.6 546 7 AA446878 zw90c04.r1 Strattgener 3.93e-19 0.6 546 7 AA112441 zm27502.r1 Strattgener 3.93e-19 0.6 546 7 AA112441 zm27502.r1 Strattagener
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14 49 0.8 330 16 AA913881 om21512.52 Soares_NFL_ 8.90e- 15 49 0.8 437 26 FR0002721 am34c11.51 Soares NFL 16 90e- 16 0.8 437 26 FR0002721 F.rubripes GSS sequenc 1.29e- 18 45 0.7 225 16 AA24261 zq89e09.r1 Stratagene 4.83e- 19 43 0.7 404 17 AA942921 EST198470 Normalized r 4.83e- 20 45 0.7 407 26 FR0002732 F.rubripes GSS sequenc 1.46e- 21 45 0.7 619 26 FR0002759 F.rubripes GSS sequenc 1.46e- 22 45 0.7 619 26 FR0002759 F.rubripes GSS sequenc 1.46e- 23 40 0.6 267 10 AA62040 ae57d03.s1 Stratagene 6.86e- 24 42 0.6 407 26 FR0002759 F.rubripes GSS sequenc 1.66e- 25 40 0.6 409 7 AA44689 zw90c04.s1 Soares tota 2.63e- 26 42 0.6 541 17 AA959928 vw58903.s1 Soares tota 2.71e- 28 39 0.6 544 17 AA959928 vw58903.s1 Soares tota 2.71e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 2.63e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.29e- 29 42 0.6 541 17 AA959928 vw58903.s1 Soares mous 3.39e- 29 42 0.6 541 17 AA988590 cugly06.y1 Soares mous 3.39e- 29 42 0.6 541 17 AA988590 cugly06.y1 Soares mous 3.39e- 29 42 0.6 541 17 AA988590 cugly06.y1 Soares mous 3.39e- 29 42 0.6 541 17 AA988300 cugly06.y1 Soares mous 3.39e- 29 42 0.5 541 17 AA988300 cugly06.y1 Soares mous 3.39e- 29 42 0.5 541 17 AA988300 cugly06.y1 Soares mous 3.39e- 20 57 52 HSZ78350 dusapiens mRNA, expres 3.37e- 26 48 0.5 54 14 AA14401 curvates 1.37e- 27 38 0.5 34 24 AA14401 curvates 3.39e- 28 39 0.5 52 HSZ78350 dusapiens mRNA, expres 3.39e- 29 55 55 55 55 55 55 55 55 55 55 55 55 55	14 49 0.8 330 16 AA913881 om21h12.52 Soares_NFL 8.90e-16 15 6.0 435 16 AA885211 am34c11.51 Soares NFL 8.90e-16 16 50 0.8 435 16 AA885211 am34c11.51 Soares NFL 8.90e-17 17 43 0.7 240 225 16 AAA214661 Exribitios GSS sequenc 1.46e-18 20 45 0.7 404 27 AAA22971 Exribitios GSS sequenc 1.46e-18 21 45 0.7 604 26 FR000275 F.rubripes GSS sequenc 1.46e-18 22 40 0.6 267 DAA62040 ae57403.51 Statemenc 1.46e-18 23 40 0.6 407 6 FR000275 F.rubripes GSS sequenc 1.46e-18 24 40 0.6 407 6 FR000275 F.rubripes GSS sequenc 2.63e-18 25 40 0.6 407 6 FR000275 F.rubripes GSS sequenc 2.64e-19
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14 9 0.8 330 16 AA913881 om21512.52 Soares_NFL_ 8.90e- 15 49 0.8 435 26 FR0002729 F.rubripes GSS sequenc 1.29e- 17 43 0.7 225 16 AA214661 zq89e09.r1 Stratagene 4.83e- 18 45 0.7 404 17 AA94291 EST198470 Normalized r 4.83e- 20 45 0.7 404 25 FR0002750 F.rubripes GSS sequenc 1.46e- 21 45 0.7 604 26 FR000273 F.rubripes GSS sequenc 1.46e- 22 45 0.7 619 26 FR0002759 F.rubripes GSS sequenc 1.46e- 23 40 0.6 57 10 AA62040 ae57603.s1 Stratagene 6.86e- 24 42 0.6 407 6 FR0002759 F.rubripes GSS sequenc 1.46e- 25 40 0.6 409 7 AA44689 rw58903.s1 Scares tota 2.63e- 26 42 0.6 541 17 AA95928 vw58903.s1 Scares for 2.63e- 27 36 0.6 541 17 AA95928 vw58903.s1 Scares for 2.63e- 28 39 0.6 58 18 AA968592 cugly06.y1 Sugano mous 2.63e- 29 42 0.6 541 17 AA95932 cugly06.y1 Sugano mous 2.63e- 29 42 0.6 541 17 AA95932 cugly06.y1 Sugano mous 2.63e- 29 42 0.6 541 17 AA95932 cugly06.y1 Sugano mous 2.63e- 29 42 0.6 541 17 AA95932 cugly06.y1 Sugano mous 2.63e- 29 42 0.6 58 18 AA988592 cugly06.y1 Sugano mous 3.93e- 26 16 18 26 FR0002754 F.rubripes GSS sequenc 2.63e- 29 42 0.6 541 17 AA959340 cugly06.y1 Sugano mous 3.93e- 26 16 18 26 FR0002754 F.rubripes GSS sequenc 2.63e- 29 42 0.6 541 17 AA959340 cugly06.y1 Sugano mous 3.93e- 26 18 18 AA799340 cugly06.y1 scares mous 3.93e- 26 18 18 AA799340 cugly06.y1 scares mous 3.93e- 26 18 27 38 26 26 H.sapiens mRNA, express 3.93e- 27 38 0.5 38 12 AA7144007 mr75D01.r1 Stratagene 1.06e- 28 0.6 541 17 AA912441 mr75D01.r1 Stratagene 1.06e- 29 0.7 540 0.7 54	14 49 0.8 330 16 AA913881 om21h12.52 Soares_NFL 15 49 0.8 435 16 AA882211 am34cll.s1 Soares NFL 16 50 0.7 437 26 FR0002729 F.rubripes GSS sequenc 1.29e-18 1.25 6 AA214661 zq89e09.r1 Stratagene 1.46e-18 1.26 0.7 386 26 FR0002750 F.rubripes GSS sequenc 1.46e-18 1.27 0.7 404 17 AA942971 EST198470 Normalized r 1.28 0.7 604 26 FR0002751 F.rubripes GSS sequenc 1.46e-18 0.7 604 26 FR0002751 F.rubripes GSS sequenc 1.46e-18 0.7 604 26 FR0002752 F.rubripes GSS sequenc 1.46e-18 0.7 619 26 FR0002759 F.rubripes GSS sequenc 1.46e-18 0.7 6 0.7
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14 9 0.8 330 16 AA8121881 om215112.52 Soarces_NFL_ 8.90e- 15 49 0.8 435 16 FRA012881 am34c11.51 Soarces_NFL_ 8.90e- 16 50 0.8 437 26 FR0002729 F.rubripes GSS sequenc 1.29e- 17 43 0.7 225 16 AA214661 zq89e09.r1 Stratagene 4.83e- 18 45 0.7 404 17 EST1884 Normalized r 4.83e- 20 45 0.7 404 17 EST1884 Normalized r 4.83e- 21 45 0.7 404 26 FR0002732 F.rubripes GSS sequenc 1.46e- 22 45 0.7 604 26 FR0002732 F.rubripes GSS sequenc 1.46e- 23 40 0.6 57 10 AA62040 ae57d03.s1 Stratagene 6.86e- 24 42 0.6 499 7 AA446897 ETUBRIPES GSS sequenc 2.63e- 25 40 0.6 541 17 AA955928 vw59004.s1 Soarces mous 2.63e- 26 42 0.6 541 17 AA955928 vw59003.s1 Soarces mous 2.63e- 27 36 0.6 58 18 AA986592 uc881906.y1 Sugano mous 3.29e- 28 39 0.6 58 18 AA986592 uc881906.y1 Sugano mous 3.39e- 29 42 0.6 619 26 FR002754 F.rubripes GSS sequenc 2.63e- 29 42 0.6 639 1 AA986592 uc881906.y1 Sugano mous 3.39e- 29 42 0.6 619 26 FR000275 F.rubripes GSS sequenc 2.63e- 29 42 0.6 619 26 FR000275 F.rubripes GSS sequenc 2.63e- 29 42 0.6 619 26 FR000275 F.rubripes GSS sequenc 2.63e- 29 42 0.6 619 26 FR000275 F.rubripes GSS sequenc 2.63e- 29 42 0.6 619 26 FR000275 F.rubripes GSS sequenc 2.63e- 29 42 0.6 619 26 FR000275 F.rubripes GSS sequenc 2.63e- 29 42 0.6 619 26 FR000275 F.rubripes GSS sequenc 2.63e- 20 714e- 20 71e- 20 71e	14 49 0.8 330 16 AA913881 om21h12.52 Soares_NFL 8.90e-16 15 49 0.8 435 16 AA88221 am34cl1.s1 Soares NFL 8.90e-17 16 50 0.7 225 16 Fr0002759 F.rubripes GSS sequenc 1.29e-18 19 45 0.7 386 26 FR0002750 F.rubripes GSS sequenc 1.46e-18 20 45 0.7 404 17 AA942971 EST198470 Normalized r 4.83e-19 21 45 0.7 604 26 FR0002759 F.rubripes GSS sequenc 1.46e-19 22 45 0.7 67 100 FR0002759 F.rubripes GSS sequenc 1.46e-19 23 40 0.6 257 10 AA620400 ae57d03.s1 Stratagene 6.86e-19 24 0.6 499 7 AA446878 xw90c04.s1 Soares mous 2.63e-19 26 42 0.6 541 7 AA446878 xw98693.s1 Soares tota 6.8e-19
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14 9 0.8 330 16 AA911881 om215112.52 Soares_NFL_ 8.90e- 15 49 0.8 435 16 FRA012891 am34c11.51 Soares_NFL_ 8.90e- 16 50 0.8 437 26 FR0002729 F.rubripes GSS sequenc 1.29e- 17 43 0.7 225 16 AA214661 zq89e09.r1 Stratagene 4.83e- 18 45 0.7 404 17 EST198470 Normalized r 4.83e- 20 45 0.7 404 17 EST198470 Normalized r 4.83e- 21 45 0.7 404 26 FR0002732 F.rubripes GSS sequenc 1.46e- 22 45 0.7 604 26 FR0002732 F.rubripes GSS sequenc 1.46e- 23 40 0.6 64 26 FR0002759 F.rubripes GSS sequenc 1.46e- 24 42 0.6 490 7 AA446897 F.rubripes GSS sequenc 6.86e- 25 40 0.6 499 7 AA446898 xw90c04.s1 Soares mous 2.63e- 26 42 0.6 541 17 AA955928 vw59g03.s1 Soares mous 2.53e- 27 36 0.6 588 18 AA986592 cc88106.v1 Suganos mous 3.27e-	14 49 0.8 330 16 AA913881 om21h12.52 Soares_NFL 8.90e-16 15 49 0.8 435 16 AA88221 am34cl1.s1 Soares NFL 8.90e-17 16 50 0.8 437 26 FR0002729 F.rubripes GSs Sequenc 1.29e-18 19 45 0.7 386 26 FR0002750 F.rubripes GSs Sequenc 1.46e-18 20 45 0.7 404 17 AA942971 EST198470 Normalized r 4.83e-19 21 45 0.7 604 26 FR0002759 F.rubripes GSs Sequenc 1.46e-19 22 45 0.7 604 26 FR0002759 F.rubripes GSs Sequenc 1.46e-19 23 40 0.6 267 10 AA620400 ae5703.s1 Stratagene 6.86e-1 24 0.6 407 26 FR0002759 F.rubripes GSs Sequenc 2.63e-1 24 0.6 407 26 FR0002759 F.rubripes GSs Sequenc 2.63e-1 25 40 <
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Marra M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marra M., Hiller, L., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                 from B.Soares,
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAAGGGGATCCGCACGCTGCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTAACA 180
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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                                                                          //solate="muscular atrophy patient"
/db_xref="taxon:9606"
/clone_lib="normalized infant brain cDNA fro
Psychiatry Dept. Columbia University USA"
/sex="female"
/tissue_type="total brain"
/dev_stage="3 months old"
3 a 78 c 80 g 112 t 5 others
                                                                                                                                                                                                                                                      Length 343;
                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 1.16e-198;
0; Mismatches 112;
Genexpress_library_idt: C;
Genexpress_sequence_idt: ylc-2hd06.
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                                                                   sapiens"
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The WashU-HHMI Mouse EST Project
                                Location/Qualifiers
                                                  1. .343
/organism="Homo
                                                                                                                                                                                                                                                   .ch 1.9%;
1 Similarity 67.3%;
231; Conservative
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AA183990
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"L' (bases 1 to 594)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba-T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/strain="C57BL/6J"
/note="Vector: pCMV-SPORT2; Site_1: Sal1; Site_2: Not1;
Cloned unidirectionally. Primer: Oligo dT. 13.5dpc
embryos. pCMV-SPORT2 vector."
/db_xref="taxon:10090"
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                                                        th LLNL ; contact the further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="615290"
/clone_lib="Life Tech mouse embryo 13 5dpc 10666014"
/dev_stage="13.5dpc embryos"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 529;
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL
IMAGE Consortium (info@image.llnl.gov) for further
MGI:376114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 4.89e-192;
0; Mismatches 93;
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High quality sequence stop: 263.
Location/Qualifiers
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Best Local Similarity 70.1%;
Matches 220; Conservative
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Centre Hinxton,
Vector: m13mp18
V_type: phage
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F.rubripes GSS sequence, clone 010M03aE5, genomic survey sequence.
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Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y.,
Halliams, G. and Brenner, S.
Direct Submission
Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
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Vettebrata: Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei;
Tetraodontidae; Fugu.
                                        Washu Hami Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:457443
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Pred. No. 4.27e-144;
0; Mismatches 58;
                                                                                                                                                                                    Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 456. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="748459"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH108"
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                                Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                1. .594 //
/organism="Mus musculus"
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GSS; genome survey sequence.
Fugu rubripes.
Fugu rubripes
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Local Similarity 73.0%;
es 157; Conservative
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Unpublished (1996)
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raws/267 413 bp mRNA EST 16-OCT-1997 ve83f11.rl Soares mouse NDMH Mus musculus cDNA clone 832845 5/ similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT (HUMAN); gb:U26707 Mus musculus voltage-gated sodium channel alpha subunit SCN8A (MOUSE);, mRNA sequence.
AA427267
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1 (bases 1 to 413)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5609 CITITIGATAGITATIAATATGIACATIGCIGICATICICGAGAACIATAGICAGGCCAC 5668
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:493061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                            cosmid cloned genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGTICGACCCAGAAGCCACACACTICATCGAGTACGCCAAGTIGTCGGACTITGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5729 GCAATTCGATCCGGAGGCACCCAGTACATACGCTATGATCAGCTGTCCGAATTCCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 CTTTCTTATCGTGGTCAACAINTACATCGCCATCATCCTGGAGAACTTCAGTGTGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 GGAGGAGGACCCCTGAGCGAGGATGACTTTGAAATGTTCTATGAGGTTTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 CTCTCTGTCAGAACCACTGCGGATCGCCAAACCTAACAAGATCAAGGTGATCTCCATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 619;
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Washington University School of MedicineP
H444 Forest Park Parkway, Box 8501, St. Louis, MO (1911: 314 286 1810)
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                      2 others
                                                                                                                                                                                                                                                                                                                                                                                                         Score 91; DB 26; Length 619
Pred. No. 5.18e-127;
0; Mismatches 105; Indels
                                                                                                                          One pass dye-terminator sequencing of
                                                                                                                                                                                                                                                                                                                                 120 t
                                                                                                                                                                                                                                                                              /clone_lib="cosmid 010M03"/clone="010M03aE5"
                                                                                                                                                                                                       1. 619
/organism="Fugu rubripes"
/db_xref="taxon:31033"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 177 g
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.4%;
Best Local Similarity 65.0%;
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                    164 c
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Fax: 314 286 1810
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                                                                                                       source
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SOURCE
ORGANISM
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                                                                                      FEATURES
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                                                                                                           AA984063 706 bp mRNA EST 27-MAY-1998 am76b09.s1 Stratageene schizo brain S11 Homo sapiens cDNA clone ILMAGE:1616345 3' similar to 9b:M94055 SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin!; Hominidae; Homo.

1 (bases 1 to 706)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marthi, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Malie, M., White, Y., Mylie, T., Materston, R. and Wilson, R. Washu. NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1185 GACTICIGGGAGGAICTGTACCAGCTGGTGTTGCGCCGCCGGCCGTGGCATGCTG 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACTACTGGGAGAACCTTTATCAACAGACACTGCGGGCTGCTGGCAAAACCTACATGATT 120
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 77; DB 10; I
Pred. No. 1.01e-97;
0; Mismatches 62;
                              Amersham
                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="832845"
/clone_lib="Soares mouse NbMH"
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                                                                                                                                                                                                                                                                                                                                                                 94
                                                                    1. .413
/organism="Mus musculus"
/strain="C57BL/6J"
            vector to vector length is
Seq primer: -28ml3 rev2 ET from ,
High quality sequence stop: 354.
                                                                                                                                                                                                                                                                                                                   /tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
a 92 c 110 g
                                                        Location/Qualifiers
Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || ||||||| |||| ||| || ||| ||| GTTGCCATGTCGTATGACGAA 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GTAGCCATGGCGTACGAGGAA 201
                                                                                                                                                                                                                                                                                                                                                                                                          1.2%;
llarity 69.2%;
Conservative
                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               706 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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93162588
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Best Local Simil
Matches 139;
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DEFINITION
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JOURNAL
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                                                        FEATURES
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AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa CADA clone 97SN1787, mRNA sequence.
AA754459 92801165
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Bukaryotae; Viridiplantae; Charophyta/Embryophyta group;

Bmbryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;

Poales; Poaceae; Oryza.

1 (bases 1 to 252)

1 (bases 1 to 252)

1 Kim, W.T., Kim, N.T., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,

Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,

Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                         /note="Vector: Bluescript SK-; Site_1: EcoRI; Library Constructed from S-11 frontal lobe, male, 34 years old, 50% caucasian, 50% Aleutian. Schizophrenic suicide. Random primed into EcoRI site of ZAP II Vector. Mass excised. Custom library. Avg insert length 1.4kb. Material obtained by Johnston N., Torrey, E.F., Yolken R. and the Stanley Neuropathology Consortium - Analysis of ENAS from the Brains of Individuals with Psychiatric Diseases (Unpublished) Stanley Neurovirology Laboratory, Johns Hopkins School of Medicine, Baltimore MD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 425.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 GCCCATGAACAACTGCAATCCTATTAGCGCAAACACGCTTAGACAGAACACAGTCAAGAT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 CATGACATCAGAAAGCTTCTTCACTGACTGGATCAGGGCACC-ACAATGGTCTTCAGGCC 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        848 AATCACATCGCGCAGATTCTTCACCGATTCGATGACGCGCCGACGACGATGTCTTCAAGCC 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         550 TGGAATGACTGAAATTGTTTTCAATGCTCGGAGAACTCTGAATGTTCTCAACGCTGAGA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
155 c 135 g 184 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1616345"
/clone_lib="Stratagene schizo brain Sll"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76; DB 18;
Pred. No. 1.15e-95;
                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          669 AATTCCATGCATCTCTAAGATACGTAAA 642
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Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 1.2%;
Local Similarity 66.0%;
Les 177; Conservative
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JOURNAL
COMMENT
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US-08-554-424-7.rst

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AA754459 252 bp mRNA EST 20-JAN-1998
97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
cDNA clone 97SN1787, mRNA sequence.
AA754459
92801165
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Eannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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seed plants; Magnoliophyta; Liliopsida;
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Bukaryotae; Viridiplantae; Charophyta/Embryophyta group;

Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida

Poales; Poaceae; Oryza.

1 (bases 1 to 252)

1 (bases 1 to 252)

1 Kim, W.T., Kim, W.Y., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,

Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,

Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .214 /organism="Homo sapiens" /organism="Homo sapiens" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5377 AAGAACGACATGCCGAAAATGGCAAAGATGAACATGACCAGGAACAGCAGCAGCAGGAGTG 5318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 TTAAACAACGCAGGAAGGGACATCATCANAGCAAAGAGCAGCGTTGCGGATCCCCTTTGC
                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research 7712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Indels
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Pred. No. 1.68e-67;
0; Mismatches 3C
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Department of Cytogenetics
National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                           Contact: Kerlavage, AR
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Similarity 75.4%;
95; Conservative
                                                                                                                                                                                                                                                                                                             Bioinformatics
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Best Local Similarity
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/organism="Oryza sativa"
/oultivar="Milyang23"
/note="vector: pBluesript SK(+); Site_1: EcoRI; Site_2:
Xho1; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="Laxon:4530"
/clone="97SNI787"

                     Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Faxil: myeun&sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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6270 CATC-CTCACCGGACTATTACATTACTCTCATCGGCATCGGCAGCTCCTTCTGCAGTA 6212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 GDWHYWBVBNTK-VDVGNHTRCSRWRBVTRWAHYHDYTNCBBYNNNDYHMWHBBMYBBTG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 CBAWMITSYBCHGNBVWVCVASHGNYMSVHNCIBRGTHCDCKNVNWSIMIWGIVNWBNVS 74
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g S g g g Cp

1; Gaps

3 others

FEATURES

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IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:685488
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin r
                                                                                                                                                    /organism="Mus musculus"
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Best Local Similarity 70.7%;
Matches 123; Conservative
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                                                                                                                                                                                        /organism="Oryza sativa"
/organism="Oryza sativa"
/oultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:430"
/clone="975N178"
/clone="975N178"
/clone="975N178"
/clone="975N178"
/clone="15" Rice Immature Seed Lambda ZAPII cDNA Library"
/clssue_type="Immature Seed"
/dev_stage="5" days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
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1 (bases 1 to 328)
Marran, Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                    Site_2:
bda ZAPII
                                                                                                                                                                                                                                                                                                                                                                        ZAPII CDNA Library"
Tel: 82 331 290 0301
Email: myeun&sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Ml3 Reverse Primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 VBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 WBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRATR 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 SYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWB 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.0%; Score 64; DB 13; Length 252
Best Local Similarity 11.6%; Pred. No. 1.92e-71;
Matches 26; Conservative 115; Mismatches 82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
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RESULT

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BASE COUNT

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DEFINITION

SOURCE ORGANISM

ACCESSION KEYWORDS REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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Contact: Harvey, D.

G. M. Rubin-Molecular and Cell Biology
University of Callfornia Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Fax: 510 643 9947
Fax: 510 cov: E column: 1
Plate: 80 row: E column: 1
High quality sequence stop: 426.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA699257 573 bp mRNA EST 18-DEC-1997 HL08049.5prime HL Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone HL08049 5prime similar to X14398: Drosophila put. sodium channel gene part 5 (AA 1320-1680), mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases I to 573)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Broksfein, P., Lewis, S. and Rubin, G.M.
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 CTTCCTCATCGTGGTCAACATGTACATTGCCATCATCCTGGAGAACTTCAGTGTGGCCAC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AGAAGAGAGCACAGAGCCCCTGAGCGAGGATGACTTCGACATGTTCTATGAGATCTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 GAAGITCGACCCGGAGC-CACCCAGITCATIGAGIAIIGGGCCCIGICCGACII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67; DB 16; I
Pred. No. 2.07e-77;
0; Mismatches 50;
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 262.
Location/Qualifiers
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,B.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
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                                                                                                                                                                                                                                                                                         5232 GGCCGTGTCGACTGGTGAAGGGAGCCAAGGGCATTCGGACACTGCTCTTCGCGTTG 5291
                                                                                                                                                                                                                                                                                                                                                                             5351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 GTAGTGTCCCTGCCCGCCCTATTTAACATCGGAGCTCTGCTAGGACTGATCACCTTTATC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
                                                                                                                                                                                                                                                                     23 GGGCGTATATTGCGGTTGATCAAGGCCGCCAAGGGGGATCAGAAAGTTGCTATTCGCTCTC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JAN-1998
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                             GCCATGTCGCTGCCGGCCCTGTTCAACATCTGCCTGCTGCTGCTTCCTGGTCATGTTCATC
                                                                                                                                                                                                                                                                                                                                                                                                              143 TACGCAATTCTGGGCATGTCGCTGTTCGGAAATGTCAAGCTCCCAGGTGCTCTCGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                  203 ATGGTGAACTTCCAGACCTTCGGGCGCA-CATGCAGTTACTGTTCCGGTTGATGACCTCA
                                                                            POT2
                                                        /clone="HL08049"
/clone_lib="HL Drosophila melanogaster head
/sex="male and female"
                                                                                                                                                                                                Score 65; DB 11; Length 573; Pred. No. 2.00e-73;
                                                                                                                                                                                                                                   0; Mismatches 100; Indels
                                                                                                           /dev_stage="head--brain & sensory organ"
/lab_host="XLI Blue"
147 c 145 g 152 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA754458 247 bp mRNA
97SN1784 Rice Immature Seed Lambda (
cDNA clone 97SN1784, mRNA sequence.
AA754458
92801164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGGGTGGAATGACGTACTTGAGTCCCTGAT 293
                                        /db_xref="taxon:7227"
                                                                                                                                                                                                1.0%;
62.9%;
                                                                                                                                                                                                                  Best Local Similarity 62.9%;
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Eun M.Y.
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AA754458 247 bp mRNA EST 20-JAN-1998 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa CDNA clone 97SN1784, mRNA sequence.
AA754458 92801164
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/cultivar="Milyang3"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xnoi; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4330"
/clone="97SNI784"
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Embryophyta, Tracheophyta, seed plants, Magnoliophyta, Liliopsida,
Poales, Poaceae, Oryza.
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Fax: 82 301 290 0307
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
                           Lambda ZAPII cDNA Library
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Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,
Kim, W.T., Kim, W.Y. Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                 2605 TIGCCAICGAGGCCACCAIGAAGCIAATGGCCAIGAGCCCCAAGTACTAITICCA-GG-A 2662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGCTGGAACATCTT-CGACTTCATTATCGTGGCCCTATCGCTATTGGAACTGGGACTCG 2721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 HCRYTVBWYYARSKYGYGTBYYSWNVDTNTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDK-TDSDCGGGCWRK 179
                                                                                                                                                                                                                                                                                                                                             1 HWDCIMNIVWRGCCCCBAWMNKHIHWMIBBWCCVRRVGTTINNGKHNGRITIWNDCSDNA 60
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 VIYGSSBYBRCGVNVMVRITSMWIDKSIKMBS-MDMSRR-SRVHYGRWMBNKKRGMSRNW
                                                                                                                                                                                                                                                                                          :
ف
                                                                                                                                                                                                                              Length 247;
                                                                                                                                                                                                169 others
                     /clone_lib="Rice Immature Seed Lambda /tissue_type="Immature Seed" /dev_stage="5 days after_pollination" /lab host="E. coli SOLR" | 16 c 21 g 34 t 169 ot
                                                                                                                                                                                                                                                                                       40; Conservative 119; Mismatches
/clone="97SN1784"
                                                                                                                                                                                                                              Query Match 0.9%;
Best Local Similarity 16.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Eun M.Y
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//organism="Homo sapiens"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_CCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soarse and M. Patima Bonaldo."
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Eukaryota: Metazoa: Chordata: Vertebrata; Mammalia: Eutheria;
Primates: Catarrhin: Hominidae; Homo.
1 (bases 1 to 330)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-11550
Email: Robert_Strausberg@inh.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. Er from Amersham
High quality: sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                  3538 GTTGCGTTATTTAGATATTTGGATTTCTTCGGCTTGTTGTTCTTCATGTCGCCTGTATC 3479
                                                                                                                                                                                                                                64 Y-TVBWYYARSKYGYGTBYYSWNVDTNTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAY 122
                                                                                                                                                                                                                                                                                                        123 CDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKVTY 182
                                                                                                                                                              5 IMNTVWRGCCCCBAWMNKH-THMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCR 63
                                                                                                                                ÷
                                                                                          Score 60; DB 13; Length 247;
                                        169 others
                                                                                                                             Indels
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
a    16 c    21 g    34 t    169 otl
                                                                                                          Pred. No. 1.36e-63;
102; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1541735"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
69 c 59 g 103 t
                                                                                                                                                                                                                                                                                                                                                                                               3478 GTGAATTCCATCCGATGGCCACCTCCAG 3444
                                                                                                                                                                                                                                                                                                                                                                          183 GSSBYBRCGVNVMVRTTSMWTDKSTKMBSMDMSRR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                          0.98;
                                                                                                          15.8%;
                                                                                                          Local Similarity 15.8%;
les 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
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/organism="Homo sapiens"
/note="Organism="Homo sapiens"
/note="Organism="Homo sapiens"
/note="Organism="Homo sapiens"
/note="Organism pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_CGB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M. G.E. clones 297480-302087, 68263-68739, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
/db_xref="texco:9606"
/clone="IMAGE:1468724"
/clone="IMAGE:1468724"
/lab_host="IMAGE:1468724"
/lab_host="Data" 136 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA885211 435 bp mRNA EST 27-MAR-1998 am34c11.s1 Scares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1468724 3' similar to TR:P70276 P70276 SODIUM CHANNEL, TYPE AA885211 g2994288
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI:Onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 390.
                                                                                                                                               5073 AAAATATTGGCTTTACGATATCACTATTTATTGAGCCATGGAATTTATTGATGTAGTA 5132
                                                                                                                                                                                                                                                                                                                                                                               196 AAAAICITIGCITIGAGGCAATACTACTICACCAAIGGCIGGAAITIATITGACIGIG 255
                                                                                                              16 CAAGGTCTCGTGTTCGACATAGTCACAAGCCAGATCTTTGACATCATCATCATAAGTCTC 75
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                           Gaps
                                                                                                                                                                                                                                                              136 TCCATCCTTGACCATCTCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
                                                              ö
  Length 330;
                                                           Indels
                                                        0; Mismatches 104;
Score 49; DB 16;
Pred. No. 8.90e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5133 GTTGTCATTTATCCAT 5149
Query Match 0.8%;
Best Local Similarity 59.5%;
Matches 153; Conservative
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Score 49; DB 16; Length 435;
Pred. No. 8.90e-43;
0; Mismatches 104; Indels
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Best Local Similarity 59.5%;
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